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184700

From: Whiteman, Brian
Sent: Monday, April 10, 2006 11:26 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09816688 High et al.

SEQ ID NO: 1

- 1) commercial database
- 2) us patents and published us patent applications

Please limit search to 20 amino acids or less

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CH1 6402 Tel: 303-4491

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 4/13
Date completed: 4/17
Searcher Prep Time: 10
Online Time: 11

Type of Search
NA# _____ AA# 1
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: 126 ✓
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____ ✓
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:49:59 ; Search time 163 Seconds
(without alignments)
15.380 Million cell updates/sec

Title: US-09-816-688B-1

Perfect score: 30

Sequence: 1 RKRRKR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Published Applications AA Main:*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	4	US-10-445-235-5
2	30	100.0	6	4	US-10-712-332-5
3	30	100.0	9	3	US-09-816-688A-1
4	30	100.0	15	5	US-10-912-764-45
5	27	90.0	8	3	US-09-876-904A-348
6	27	90.0	8	4	US-10-028-056-25
7	27	90.0	8	4	US-10-211-088-230
8	27	90.0	8	5	US-10-482-029-359
9	27	90.0	12	3	US-09-933-780C-35
10	27	90.0	13	3	US-09-746-170-39
11	27	90.0	19	4	US-10-225-567A-1183
12	27	90.0	21	3	US-09-864-761-48960
13	26	86.7	8	4	US-10-057-620-7
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103 Sequence 151, App
104 Sequence 157, App
105 Sequence 349, App
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142 Sequence 426, App
143 Sequence 89, Appl
144 Sequence 4, Appl
145 Sequence 5, Appl
146 Sequence 27, Appl
147 Sequence 152, App
148 Sequence 158, App
149 Sequence 13, Appl
150 Sequence 5, Appl
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ALIGNMENTS

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RESULT 1
US-10-445-235-5
; Sequence 5, Application US/10445235
; Publication No. US20040005670A1
; GENERAL INFORMATION:
; APPLICANT: Katherine A. High
; APPLICANT: Rodney M. Camire
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF HEMOPHILIA A
; FILE REFERENCE: CHOP0176
; CURRENT APPLICATION NUMBER: US/10/445,235
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: 60/382,486
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 6
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-445-235-5

Query Match 100.0%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRKR 6
Db 1 RRRKR 6

RESULT 2
US-10-712-332-5
; Sequence 5, Application US/10712332
; Publication No. US20040072757A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; Sinha, Uma
; TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan, Lewis & Bockius LLP
; STREET: 1111 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/712,332
; FILING DATE: 13-Nov-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,346
; FILING DATE: 27-Sep-2000
; APPLICATION NUMBER: US 07/578,646
; FILING DATE: 1990-09-04
; APPLICATION NUMBER: US 07/808,329
; FILING DATE: 1991-12-16
; APPLICATION NUMBER: US 08/249,777
; FILING DATE: 1994-05-26
; APPLICATION NUMBER: US 08/268,003
; FILING DATE: 1994-06-29
; APPLICATION NUMBER: US 08/469,301
; FILING DATE: 1995-06-06
; APPLICATION NUMBER: US 09/016,403
; APPLICATION NUMBER: US 09/362,207
; FILING DATE: 1999-07-28
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael S. Tuscan, Ph.D.
; REGISTRATION NUMBER: 43,210
; REFERENCE/DOCKET NUMBER: 44481-5002-15-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 739-3000
; TELEFAX: (202) 739-3001
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-712-332-5

Query Match 100.0%; Score 30; DB 4; Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

RESULT 3

US-09-816-688A-1
; Sequence 1, Application US/09816688A
; Publication No. US20040102388A1
; GENERAL INFORMATION:
; APPLICANT: THE CHILDREN'S HOSPITAL OF PHILADELPHIA
; APPLICANT: HIGH, KATHERINE
; APPLICANT: MARGARITAS, PARIS
; APPLICANT: CAMRIE, RODNEY
; TITLE OF INVENTION: MODIFIED BLOOD CLOTTING FACTORS AND METHODS OF USE
; FILE REFERENCE: 018743-0278737
; CURRENT APPLICATION NUMBER: US/09/816,688A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,331
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic proteolytic cleavage
; OTHER INFORMATION: peptide
US-09-816-688A-1

Query Match 100.0%; Score 30; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

RESULT 4

US-10-912-764-45
; Sequence 45, Application US/10912764
; Publication No. US20050059122A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; TITLE OF INVENTION: TARGETED CARRIER FUSIONS FOR DELIVERY OF
; FILE REFERENCE: WARP:011US
; CURRENT APPLICATION NUMBER: US/10/912,764
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 60/492,508
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-912-764-45

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Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

DB 5 RRRRR 10

RESULT 5

US-09-876-904A-348
; Sequence 348, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 348
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse Oct-2 protein transcription factors (Oct-2.1
; OTHER INFORMATION: for Oct-2.6 isoforms)
US-09-876-904A-348

Query Match 90.0%; Score 27; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 2 RRRRR 7

RESULT 6

US-10-028-056-25
; Sequence 25, Application US/10028056
; Publication No. US20020152483A1
; GENERAL INFORMATION:
; APPLICANT: REUE, KAREN
; APPLICANT: PTERFY, MIKLOS
; TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN
; FILE REFERENCE: 407T-898010US
; CURRENT APPLICATION NUMBER: US/10/028,056
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,772
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-056-25

Query Match 90.0%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

RESULT 7

US-10-211-088-230
; Sequence 230, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.

```

; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
; US-10-211-088-230

Query Match          90.0%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
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Db 2 RKRRKR 7

RESULT 8
US-10-482-029-359
; Sequence 359, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-482-029-359

Query Match          90.0%; Score 27; DB 5; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 2 RKRRKR 7

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US-09-933-780C-35
; Sequence 35, Application US/09933780C
; Publication No. US20030229202A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07

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Best Local Similarity 83.3%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
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Db 5 RRRKR 10

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US-09-864-761-48960

; Sequence 48960, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864, 761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

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; PRIOR APPLICATION NUMBER: PCT/US01/00668

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; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 48960

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC008171.1

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.62

US-09-864-761-48960

Query Match 90.0%; Score 27; DB 3; Length 21;

Best Local Similarity 83.3%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 10 RKRRR 15

RESULT 13

US-10-057-620-7

; Sequence 7, Application US/10057620

; Publication No. US20030229036A1

; GENERAL INFORMATION:

; APPLICANT: GENZYME CORPORATION

; APPLICANT: Scaria, Abraham

; APPLICANT: Wadsworth, Samuel C.

; TITLE OF INVENTION: METHODS FOR TREATING BLOOD COAGULATION DISORDERS

; FILE REFERENCE: 5046US

; CURRENT APPLICATION NUMBER: US/10/057,620

; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: PCT/US01/51391

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/307,492

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: US 60/243,046

; PRIOR FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-620-7

Query Match 86.7%; Score 26; DB 4; Length 8;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 1 RKRRKR 6

RESULT 14

US-10-902-959-49

; Sequence 49, Application US/10902959

; Publication No. US20050059595A1

; GENERAL INFORMATION:

; APPLICANT: MCKERRACHER, LISA

; TITLE OF INVENTION: FUSION PROTEINS

; FILE REFERENCE: 06746-004-US-03

; CURRENT APPLICATION NUMBER: US/10/902,959

; CURRENT FILING DATE: 2004-08-02

; PRIOR APPLICATION NUMBER: CA 2,367,636

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: CA 2,362,004

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: CA 2,342,970

; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 49

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence fused to C3 protein to created C3 Tat-short

US-10-902-959-49

Query Match 86.7%; Score 26; DB 5; Length 10;

Best Local Similarity 83.3%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 3 RKRRR 8

```

; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-25

Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
        |||:|
DB      2 RKQKR 7

RESULT 18
US-09-746-170-31
; Sequence 31, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-31

Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
        |||:|
DB      2 RKQKR 7

RESULT 19
US-09-746-170-35
; Sequence 35, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-35

```


Query Match 86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 RKRKR 6
Db 2 RKRKRQ 7

RESULT 20

US-09-746-170-37
; Sequence 37, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-37

Query Match 86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 RKRKR 6
Db 2 RKRQR 7

RESULT 21

US-10-983-169-3
; Sequence 3, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-100012
; CURRENT APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,502
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Apis mellifera
US-10-983-169-3

Query Match 86.7%; Score 26; DB 5; Length 15;
Best Local Similarity 83.3%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 RKRKR 6
Db 2 RKRQR 7

RESULT 22

US-10-983-169-10
; Sequence 10, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-100012
; CURRENT APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,502
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cys-Mel-Ova 257-64
US-10-983-169-10

Query Match 86.7%; Score 26; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 RKRKR 6
Db 3 RKRQR 8

RESULT 23

US-09-809-790-7
; Sequence 7, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bairdur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-790-7

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 RKRKR 6
Db 1 RKRKR 5

RESULT 24

US-09-809-790-8
; Sequence 8, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bairdur, Nand
; APPLICANT: Deisher, Theresa A.

```
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-790-8

Query Match      83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KRRKR 6
Db      2 KRRKR 6

RESULT 25
US-09-809-617-7
; Sequence 7, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-617-7

Query Match      83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KRRKR 6
Db      1 KRRKR 5

RESULT 26
US-09-809-617-8
; Sequence 8, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; .

; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-617-8

Query Match      83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KRRKR 6
Db      2 KRRKR 6

RESULT 27
US-09-876-904A-360
; Sequence 360, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human PRDII-BF1 that binds to IFN-beta gene
; OTHER INFORMATION: promoter.
US-09-876-904A-360

Query Match      83.3%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KRRRK 5
Db      2 KRRRK 6

RESULT 28
US-10-660-370-194
; Sequence 194, Application US/10660370
; Publication No. US20050064507A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, J. Stephen
; APPLICANT: National Institutes of Health
; TITLE OF INVENTION: Determining Kinase Specificity
; FILE REFERENCE: 1662.009US2
; CURRENT APPLICATION NUMBER: US/10/660,370
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 640
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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Job time : 164 secs

; OTHER INFORMATION: A synthetic peptide
US-10-660-370-194

Query Match 83.3%; Score 25; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 6
DB 1 KRRK 5

RESULT 29
US-09-746-170-8
; Sequence 8, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-8

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRK 5
DB 6 KRRK 10

RESULT 30
US-09-746-170-17
; Sequence 17, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-17

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRK 5
DB 6 KRRK 10

Search completed: April 13, 2006, 08:53:22

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:41:39 ; Search time 184 Seconds
(without alignments)
14.328 Million cell updates/sec

Title: US-09-816-688b-1
Perfect score: 30
Sequence: 1 RKRRKR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	AAU09934	Aau09934 Synthetic
2	30	100.0	6	ADP09125	Adp09125 PACE-furi
3	30	100.0	8	ADK08902	Adk08902 Human pap
4	30	100.0	9	AAW42225	Aar42225 Anti-herp
5	30	100.0	9	AAW70502	Aar70502 Anti-herp
6	30	100.0	9	AAW24810	Aaw24810 Anti-herp
7	30	100.0	9	AAW25615	Aaw25615 Peptide #
8	30	100.0	9	ABR07953	AbR07953 Human can
9	30	100.0	9	ABR08153	AbR08153 Human can
10	30	100.0	9	ABR08722	AbR08722 Human can
11	30	100.0	9	ABR07954	AbR07954 Human can
12	30	100.0	9	ABR08474	AbR08474 Human can
13	30	100.0	9	ABR08536	AbR08536 Human can
14	30	100.0	9	ABR08558	AbR08558 Human can
15	30	100.0	9	ABR08701	AbR08701 Human can
16	30	100.0	9	ABR07558	AbR07558 Human can
17	30	100.0	9	ABR08154	AbR08154 Human can
18	30	100.0	9	ADK08966	Adk08966 Human pap
19	30	100.0	10	ABR08921	AbR08921 Human can
20	30	100.0	10	ABR08402	AbR08402 Human can
21	30	100.0	10	ABR08569	AbR08569 Human can
22	30	100.0	10	ABR08053	AbR08053 Human can
23	30	100.0	10	ABR08455	AbR08455 Human can
24	30	100.0	10	ABR08599	AbR08599 Human can

25	30	100.0	10	ABR07978	Human can
26	30	100.0	10	ABR08871	Human can
27	30	100.0	10	ABR08821	Human can
28	30	100.0	10	ABR08771	Human can
29	30	100.0	10	ABR08212	Human can
30	30	100.0	10	ABR07803	Human can
31	30	100.0	10	ABR07601	Human can
32	30	100.0	10	ABR08196	Human can
33	30	100.0	10	ABR08253	Human can
34	30	100.0	10	ADK09033	Human pap
35	30	100.0	10	ADK09030	Human pap
36	30	100.0	10	ADK09031	Human pap
37	30	100.0	10	ADK09032	Human pap
38	30	100.0	11	ABP54087	Abp54087 Transpore
39	30	100.0	11	ADC19832	Adc19832 Fluoresce
40	30	100.0	15	ABR32392	Human can
41	30	100.0	15	ABR32483	Human can
42	30	100.0	15	ABR32427	Human can
43	30	100.0	15	ABR32527	Human can
44	30	100.0	15	ABR32391	Human can
45	30	100.0	15	ABR32528	Human can
46	30	100.0	15	ADK58977	Human can
47	30	100.0	18	ABR11544	AbR11544 Apolipop
48	30	100.0	21	AAW79064	AAW79064 Peptide w
49	27	90.0	6	ABR57040	AbR57040 Furin-rec
50	27	90.0	6	ABR74584	AbB74584 Transcrip
51	27	90.0	8	ADG27383	AdG27383 Lipin nuc
52	27	90.0	8	ADG22381	AdG22381 Nuclear l
53	27	90.0	8	ADG22381	AdG22381 Nuclear l
54	27	90.0	8	ADG22381	AdG22381 Nuclear l
55	27	90.0	8	ADG22381	AdG22381 Nuclear l
56	27	90.0	8	ADG22381	AdG22381 Nuclear l
57	27	90.0	8	ADG22381	AdG22381 Nuclear l
58	27	90.0	8	ADG22381	AdG22381 Nuclear l
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78	27	90.0	8	ADG22381	AdG22381 Nuclear l
79	27	90.0	8	ADG22381	AdG22381 Nuclear l
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81	27	90.0	8	ADG22381	AdG22381 Nuclear l
82	27	90.0	8	ADG22381	AdG22381 Nuclear l
83	27	90.0	8	ADG22381	AdG22381 Nuclear l
84	27	90.0	8	ADG22381	AdG22381 Nuclear l
85	27	90.0	8	ADG22381	AdG22381 Nuclear l
86	27	90.0	8	ADG22381	AdG22381 Nuclear l
87	27	90.0	8	ADG22381	AdG22381 Nuclear l
88	27	90.0	8	ADG22381	AdG22381 Nuclear l
89	27	90.0	8	ADG22381	AdG22381 Nuclear l
90	27	90.0	8	ADG22381	AdG22381 Nuclear l
91	27	90.0	8	ADG22381	AdG22381 Nuclear l
92	27	90.0	8	ADG22381	AdG22381 Nuclear l
93	27	90.0	8	ADG22381	AdG22381 Nuclear l
94	27	90.0	8	ADG22381	AdG22381 Nuclear l
95	27	90.0	8	ADG22381	AdG22381 Nuclear l
96	27	90.0	8	ADG22381	AdG22381 Nuclear l
97	27	90.0	8	ADG22381	AdG22381 Nuclear l

98 27 90.0 21 4 ABB32457
 99 26 86.7 7 6 AAO16743
 100 26 86.7 8 5 ABG11280
 101 26 86.7 10 4 AAG86255
 102 26 86.7 10 9 AD225756
 103 26 86.7 10 9 AEA47550
 104 26 86.7 11 3 AAB30411
 105 26 86.7 11 9 AEA47559
 106 26 86.7 13 3 AAY69769
 107 26 86.7 13 3 AAY69765
 108 26 86.7 13 3 AAY69771
 109 26 86.7 13 3 AAY69760
 110 26 86.7 13 4 AAU06106
 111 26 86.7 13 4 AAU06097
 112 26 86.7 13 4 AAU06108
 113 26 86.7 13 4 AAU06102
 114 26 86.7 13 8 ADU15719
 115 26 86.7 15 9 AEA47551
 116 26 86.7 18 9 AEB11553
 117 26 86.7 19 9 AEA47558
 118 25 83.3 5 2 AAW26219
 119 25 83.3 5 6 AAE33758
 120 25 83.3 6 3 AAY54459
 121 25 83.3 6 3 AAY54458
 122 25 83.3 6 4 AAU07191
 123 25 83.3 6 4 AAU07192
 124 25 83.3 6 5 ABB78131
 125 25 83.3 6 5 ABB78132
 126 25 83.3 6 9 AEA41490
 127 25 83.3 6 9 AEA41455
 128 25 83.3 6 9 AEA42006
 129 25 83.3 6 9 AEA41454
 130 25 83.3 6 9 AEA41496
 131 25 83.3 6 9 AEA42007
 132 25 83.3 7 2 AAY05442
 133 25 83.3 8 2 AAW02277
 134 25 83.3 8 5 ABB74596
 135 25 83.3 8 8 ADK08903
 136 25 83.3 8 9 AEA42005
 137 25 83.3 8 9 AEA41486
 138 25 83.3 9 2 AAR05609
 139 25 83.3 9 6 ABR07493
 140 25 83.3 9 6 ABR07871
 141 25 83.3 9 6 ABR08071
 142 25 83.3 9 8 ADK08968
 143 25 83.3 9 8 ADK08967
 144 25 83.3 10 6 ABR08637
 145 25 83.3 10 6 ABR07588
 146 25 83.3 10 6 ABR08008
 147 25 83.3 10 6 ABR08183
 148 25 83.3 10 8 ADK09035
 149 25 83.3 10 8 ADK09034
 150 25 83.3 11 2 AAR28129

ALIGNMENTS

RESULT 1
 AAU09934
 ID AAU09934 standard; peptide; 6 AA.
 XX
 AC AAU09934;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Synthetic proteolytic cleavage recognition site peptide sequence #1.
 KW Proteolytic cleavage recognition site; haemostatic; factor VII-agonist;
 KW factor VIII-agonist; factor IX-agonist; modified blood clotting factor;
 KW MBGF; bleeding disorder; clotting disorder; Factor VII; Factor VIII;
 KW Factor IX; vitamin-K dependent procoagulant; platelet aggregation;
 KW haemophilia; Glanzmann's thrombasthenia; antibody; immunogenicity;

KW Bernard-Soulier's thrombasthenia; decreased clotting time.
 XX Synthetic.
 OS WO200170763-A1.
 PN 27-SEP-2001.
 PD 22-MAR-2001; 2001WO-US009355.
 XX 22-MAR-2000; 2000US-0191331P.
 XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 PA High KA, Margaritis P, Camire RM;
 PI WPI; 2001-611468/70.
 DR Mutant blood clotting factors useful for treating a bleeding or clotting
 PT disorder in a subject, comprising a modified proteolytic cleavage site
 PT not normally present in the factor.
 XX Claim 9; Page 41; 55pp; English.
 PS The invention relates to a new composition comprising a recombinant
 CC polynucleotide that encodes a modified blood clotting factor (MBGF),
 CC where the modification comprises a proteolytic cleavage site not normally
 CC present in the factor, and where the factor is cleaved at the cleavage
 CC site when expressed in an animal cell. The new composition is useful for
 CC treating a bleeding or clotting disorder of a subject, preferably mammal
 CC especially human, having or at risk of having such a disorder, amenable
 CC to treatment with Factor VII, Factor VIII or Factor IX and caused by
 CC insufficient activity of expression of a vitamin-K dependent
 CC procoagulant, or by insufficient platelet aggregation. The disorder
 CC comprises haemophilia comprising haemophilia A or B, or Factor VII
 CC deficiency, Glanzmann's thrombasthenia or Bernard-Soulier's
 CC thrombasthenia. The subject produces inhibitory antibodies that bind to a
 CC clotting factor preferably Factor VIII or Factor IX. The composition of
 CC the invention is also useful for decreasing clotting time and for
 CC reducing the frequency or severity of bleeding in a subject. Unlike wild
 CC type Factor VII, MBGF comprises a Factor VII having increased activity,
 CC increased stability and decreased immunogenicity in vivo; and the
 CC secretion of the cleaved factor eliminates proteolytic cleavage during
 CC the blood clotting process. The present peptide sequence represents a
 CC synthetic proteolytic cleavage recognition site of the invention
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 30; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRKR 6
 |||||
 Db 1 RRRKR 6
 RESULT 2
 ADF09125
 ID ADF09125 standard; peptide; 6 AA.
 XX
 AC ADF09125;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE PACE-furin-like protease cleavage site peptide SEQ ID NO:5.
 XX human; factor VIII; FVIII; variant; haemostatic; gene therapy;
 KW haemophilia.
 KW Synthetic.
 OS WO2003100053-A1.
 PN

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XX PD 04-DEC-2003.
XX PF 22-MAY-2003; 2003WO-US016376.
XX PS 22-MAY-2002; 2002US-0382486P.
XX PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX PI High KA, Camire RM;
XX WPI; 2004-035147/03.
XX New nucleic acid sequence encoding a biologically active recombinant
PT human factor VIII variant, useful for preparing a composition for
PT treating hemophilia.
XX Claim 3; SEQ ID NO 5; 57pp; English.
XX The present invention describes an isolated nucleic acid sequence
CC encoding a biologically active recombinant human factor VIII (FVIII)
CC variant comprising variants set forth in table 2 in the specification
CC (see page 32-33). Also described: (1) a vector comprising the nucleic
CC acid sequence; (2) an isolated modified human FVIII protein produced by
CC expression of the nucleic acid; and (3) a method of treating haemophilia
CC in a patient. Human FVIII has haemostatic activity, and can be used in
CC gene therapy. The nucleic acid can be used for preparing a composition
CC for treating haemophilia. The present sequence represents a PACB-furin-
CC like protease cleavage site peptide, which is used in the exemplification
CC of the present invention. The human FVIII gene is located on chromosome
CC X, more specifically to Xq28.
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 30; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. NO. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
DB 1 RKRRKR 6
RESULT 3
ADK08902
ID ADK08902 standard; peptide; 8 AA.
XX AC ADK08902;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #957.
XX pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX WO2004011650-A2.
XX PD 05-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EP008112.
XX 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX (INTE-) INTERCELL AG.
XX Mattner F, Schmidt W, Habel A;
XX WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
XX preventing an infection with the pathogenic virus.
PS Claim 18; Page 184; 220pp; English.
XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX invention.
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 30; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. NO. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
DB 2 RKRRKR 7
RESULT 4
AAR42225
ID AAR42225 standard; peptide; 9 AA.
XX AC AAR42225;
XX DT 25-MAR-2003 (revised)
XX DT 17-MAY-1994 (first entry)
XX DE Anti-herpetic peptide.
XX Treatment; herpes virus infection; antiherpetic.
XX OS Synthetic.
XX WO9321941-A1.
XX PD 11-NOV-1993.
XX PF 21-APR-1993; 93WO-CA000166.
XX PR 23-APR-1992; 92US-00872398.
XX (KIRW/) KIRWOOD S D.
XX (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.
XX Twist M, Barnett RW, Summer-Smith M;
XX WPI; 1993-368410/46.
XX Compens. for treatment of herpes virus infections - contg.
PT oligopeptide(s), esp. nona:D-arginine peptide, as active agent.
XX Disclosure; Page 9; 36pp; English.
XX The peptide may be used in a compen. for the treatment of herpes virus
CC infection in humans or animals, this may be administered topically or
CC systemically. The peptide is prepd. by conventional methods, e.g., by
CC solid phase synthesis methods. (Updated on 25-MAR-2003 to correct PN
CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. NO. 2e+06;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 2 RRRRR 7

RESULT 5
AAW70502
ID AAW70502 standard; peptide; 9 AA.
XX
AC AAW70502;
XX
DT 04-JAN-1996 (first entry)
XX
DE Anti-cytomegalovirus peptide.
XX
KW Anti-cytomegalovirus; CMV; gancyclovir; foscarnet; AIDS; chemotherapy;
KW tissue rejection therapy; treatment.
XX
OS Synthetic.
XX
PN W09511038-A1.
XX
PD 27-APR-1995.
XX
PF 21-OCT-1994; 94WO-CA000590.
XX
PR 22-OCT-1993; 93US-00139757.
XX
PA (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Twist M, Summer-Smith M;
XX
DR WPI; 1997-309327/28.
XX
PT New cationic peptide rich in D-arginine residues - useful for treating
PT cytomegalovirus infections, e.g. in immuno-compromised AIDS patients.
XX
PS Disclosure; Col 19; 20pp; English.
XX
CC Peptides AAW24802-26 are examples of peptides of formula: R1-X-R2, where
CC R1 = H or a N-terminal protecting group, especially an acyl group; R2 =
CC OH or a C-terminal protecting group, especially an amide group; and X is
CC an oligopeptide chain of 'n' D-amino acid residues. The oligopeptide
CC preferably has a net positive charge of n, n-1 or n-2. It comprises D-Arg
CC residues with a maximum of 3 other D-residue. The peptides are used for
CC treating cytomegalovirus infections in immunocompromised patients,
CC especially AIDS patients. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 2 RRRRR 7

RESULT 6
AAW24810
ID AAW24810 standard; peptide; 9 AA.
XX
AC AAW24810;
XX
DT 25-MAR-2003 (revised)
DT 09-OCT-1997 (first entry)
XX
DE Anti-cytomegalovirus peptide #9.
XX
KW Cytomegalovirus; infection; immunocompromised patient; AIDS;
KW acquired immunodeficiency syndrome.
XX
OS Synthetic.

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XX FH Key Location/Qualifiers
XX FT Misc-difference 1..9
XX FT /note= "D-form residues; the N-terminal residue is
XX FT preferably acylated and the C-terminal residue is
XX FT preferably amidated"
XX
XX PN US5633230-A.
XX
XX PD 27-MAY-1997.
XX
XX PF 31-OCT-1994; 94US-00332518.
XX
XX PR 24-OCT-1990; 90US-00602953.
XX PR 23-OCT-1991; 91US-00779735.
XX PR 23-APR-1992; 92US-00872398.
XX PR 22-DEC-1992; 92US-00995742.
XX PR 22-OCT-1993; 93US-00139757.
XX
XX PA (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
XX
XX PI Twist M, Summer-Smith M;
XX
XX DR WPI; 1997-309327/28.
XX
XX PT New cationic peptide rich in D-arginine residues - useful for treating
XX PT cytomegalovirus infections, e.g. in immuno-compromised AIDS patients.
XX
XX PS Disclosure; Col 19; 20pp; English.
XX
XX CC Peptides AAW24802-26 are examples of peptides of formula: R1-X-R2, where
XX CC R1 = H or a N-terminal protecting group, especially an acyl group; R2 =
XX CC OH or a C-terminal protecting group, especially an amide group; and X is
XX CC an oligopeptide chain of 'n' D-amino acid residues. The oligopeptide
XX CC preferably has a net positive charge of n, n-1 or n-2. It comprises D-Arg
XX CC residues with a maximum of 3 other D-residue. The peptides are used for
XX CC treating cytomegalovirus infections in immunocompromised patients,
XX CC especially AIDS patients. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 2 RRRRR 7

RESULT 7
AAW25615
ID AAW25615 standard; peptide; 9 AA.
XX
XX AC AAW25615;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-NOV-1997 (first entry)
XX
XX DE Peptide #10, inhibits HIV replication.
XX
XX KW Inhibition; HIV; human immunodeficiency virus; replication.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..9
XX FT /note= "Opt. D-form residues"
XX
XX PN US5646120-A.
XX
XX PD 08-JUL-1997.

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PF 14-DEC-1994; 94US-00357056.
 PR 24-OCT-1990; 90US-00602953.
 PR 23-OCT-1991; 91US-00779735.
 XX (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA Sonenberg N, Reid LS, Barnett RW, Sumner-Smith M;
 XX WPI; 1997-362969/33.
 DR New D-arginine oligomers - useful as antiviral agents, especially against
 XX HIV.
 PT Disclosure; Col 6; 14pp; English.
 PS The sequences given in AA25606-33 represent peptides which can be used
 CC in D-Arginine oligomers of formula: R1-X-R2 (I). R1 = H, lower alkanoyl,
 CC a deaminated amino acid or a N-terminal protecting group; R2 = OH, lower
 CC alkyl, amino, mono- or di(lower alkyl)amino, a decarboxylated amino acid
 CC or a C-terminal protecting group; X = a chain of 7-12 D-arginine
 CC residues. The compounds are useful as antiviral agents, especially for
 CC inhibiting HIV replication. They are administered in intravenous doses of
 CC 1 microg/kg to 10 mg/kg, especially 0.1-5 mg/kg. (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 30; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRRR 6
 DB |||||
 2 RRRRR 7
 RESULT 8
 ABR07953
 ID ABR07953 standard; peptide; 9 AA.
 AC ABR07953;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 151PIC7A HLA peptide #488.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283921-A2.
 PN 24-OCT-2002.
 PD 10-APR-2002; 2002WO-US011654.
 PF 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 191; 1021pp; English.
 PS The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRRRR 6
 DB |||||
 4 RRRRR 9
 RESULT 9
 ABR08153
 ID ABR08153 standard; peptide; 9 AA.
 AC ABR08153;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 151PIC7A HLA peptide #688.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283921-A2.
 PN 24-OCT-2002.
 PD 10-APR-2002; 2002WO-US011654.
 PF 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 193; 1021pp; English.
 PS The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
 Db 4 RRRKR 9

RESULT 10
 ABR08722
 ID ABR08722 standard; peptide; 9 AA.
 AC ABR08722;
 XX
 DT 19-MAY-2003 (first entry)
 DE Human cancer-related protein 151P1C7A HLA peptide #1257.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.

OS
 XX WO200283921-A2.
 PN
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 PA (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 199; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRRKR 6
 Db 3 RRRKR 8

RESULT 11
 ABR07954
 ID ABR07954 standard; peptide; 9 AA.

XX ABR07954;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 151P1C7A HLA peptide #489.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 191; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
 Db 1 RRRKR 6

RESULT 12
 ABR08474
 ID ABR08474 standard; peptide; 9 AA.

XX ABR08474;
 AC
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #1009.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0283112P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI
 XX WPI; 2003-075555/07.
 XX
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 XX Claim 13; Page 197; 1021pp; English.
 PS
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 3 RKRRKR 8
 XX
 RESULT 13
 ABR08536
 ID ABR08536 standard; peptide; 9 AA.
 AC
 XX ABR08536;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #1071.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX

OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0283112P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI
 XX WPI; 2003-075555/07.
 XX
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 XX Claim 13; Page 197; 1021pp; English.
 PS
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 2 RKRRKR 7
 XX
 RESULT 14
 ABR08558
 ID ABR08558 standard; peptide; 9 AA.
 AC
 XX ABR08558;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #1093.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 XX

PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
DR
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 197; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
Db 4 RKRRKR 9
RESULT 15
ABR08701
ID ABR08701 standard; peptide; 9 AA.
AC ABR08701;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 151P1C7A HLA peptide #1236.
DE Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
KW Homo sapiens.
XX WO200283921-A2.
PN 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
DR New composition comprising a substance that modulates the structure of
XX

PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 199; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
Db 2 RKRRKR 7
RESULT 16
ABR07558
ID ABR07558 standard; peptide; 9 AA.
XX ABR07558;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 151P1C7A HLA peptide #93.
DE Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX WO200283921-A2.
PN 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011654.
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 187; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 4 RKRRKR 9

RESULT 17
 ABR08154
 ID ABR08154 standard; peptide; 9 AA.

AC ABR08154;
 DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 151P1C7A HLA peptide #689.
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.

OS
 PN WO200283921-A2.
 PD 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011654.
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.
 PA

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX

PS Claim 13; Page 193; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ASZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 1 RKRRKR 6

RESULT 18
 ADK08966
 ID ADK08966 standard; peptide; 9 AA.

AC ADK08966;
 DT 06-MAY-2004 (first entry)

DE Human papillomavirus peptide #1021.
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.

OS Human papillomavirus.
 PN WO2004011650-A2.

PD 05-FEB-2004.

PF 24-JUL-2003; 2003WO-EP008112.
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

PI Mattner F, Schmidt W, Habel A;
 PI WPI; 2004-169243/16.

XX New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX

PS Claim 18; Page 184; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 3 RKRRKR 8

RESULT 19
 ABR08921
 ID ABR08921 standard; peptide; 10 AA.

XX ABR08921;
 AC

```

XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #1456.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC PT diagnostic reagents for eliciting cellular or humoral immune response in
XX CC PT cancer patients.
XX PS Claim 13; Page 201; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX Query Match 100.0%; Score 30; DB 6; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 86;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 4 RRRKR 9
RESULT 20
ABR08402
ID ABR08402 standard; peptide; 10 AA.
XX AC ABR08402;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #937.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC PT diagnostic reagents for eliciting cellular or humoral immune response in
XX CC PT cancer patients.
XX PS Claim 13; Page 201; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX Query Match 100.0%; Score 30; DB 6; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 86;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 4 RRRKR 9
RESULT 21
ABR08569
ID ABR08569 standard; peptide; 10 AA.
XX AC ABR08569;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #1104.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC PT diagnostic reagents for eliciting cellular or humoral immune response in
XX CC PT cancer patients.
XX PS Claim 13; Page 196; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX Query Match 100.0%; Score 30; DB 6; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 86;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 3 RRRKR 8
RESULT 21
ABR08569
ID ABR08569 standard; peptide; 10 AA.
XX AC ABR08569;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #1104.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC PT diagnostic reagents for eliciting cellular or humoral immune response in
XX CC PT cancer patients.
XX PS Claim 13; Page 196; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX Query Match 100.0%; Score 30; DB 6; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 86;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 3 RRRKR 8

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PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 198; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 3 RKRRKR 8

RESULT 22
 ABR08053
 ID ABR08053 standard; peptide; 10 AA.
 XX ABR08053;
 AC ABR08053;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 151P1C7A HLA peptide #588.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200283921-A2.
 PD 24-OCT-2002.
 PF 10-APR-2002; 2002WO-US011654.
 XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

PT cancer patients.
 XX Claim 13; Page 192; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 2 RKRRKR 7

RESULT 23
 ABR08455
 ID ABR08455 standard; peptide; 10 AA.
 XX ABR08455;
 AC ABR08455;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 151P1C7A HLA peptide #990.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200283921-A2.
 PD 24-OCT-2002.
 PF 10-APR-2002; 2002WO-US011654.
 XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 196; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC diagnostic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 4 RRRKR 9

RESULT 24
ABR08599
ID ABR08599 standard; peptide; 10 AA.

XX ABR08599;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1134.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.

XX 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX Claim 13; Page 198; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
Db 4 RRRKR 9

RESULT 25
ABR07978
ID ABR07978 standard; peptide; 10 AA.

XX ABR07978;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #513.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.

XX 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX Claim 13; Page 192; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 5 RRRKR 10

RESULT 26
ABR08871

ID	ABR08871	standard; peptide; 10 AA.	
XX	OS	Homo sapiens.	
AC	ABR08871;		
XX	DT	19-MAY-2003 (first entry)	
DE	DE	Human cancer-related protein 151P1C7A HLA peptide #1406.	
KW	KW	Human; cytostatic; vaccine; cancer; immune response; HLA;	
XX	XX	human leukocyte antigen.	
OS	OS	Homo sapiens.	
PN	PN	WO200283921-A2.	
XX	PD	24-OCT-2002.	
XX	XX	10-APR-2002; 2002WO-US011654.	
PR	PR	10-APR-2001; 2001US-0282739P.	
PR	PR	10-APR-2001; 2001US-0283112P.	
PR	PR	25-APR-2001; 2001US-0286630P.	
XX	XX	(AGEN-) AGENSYS INC.	
PA	PA	Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;	
XX	PI	Morrison K, Morrison RK, Raitano AB;	
XX	PI	WPI; 2003-075555/07.	
XX	DR	New composition comprising a substance that modulates the structure of	
XX	PT	proteins and polynucleotides, useful for therapeutic, prognostic and	
XX	PT	diagnostic reagents for eliciting cellular or humoral immune response in	
XX	PT	cancer patients.	
XX	XX	Claim 13; Page 201; 1021pp; English.	
XX	PS	The present invention relates to novel human cancer-related genes and	
XX	CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and	
XX	CC	proteins are useful for eliciting a humoral or cellular immune response.	
XX	CC	The genes are useful as probes and primers for the amplification and/or	
XX	CC	detection of genes, mRNAs or their fragments, as reagents for the	
XX	CC	diagnosis and/or prognosis of cancer, as coding sequences capable of	
XX	CC	directing the expression of the protein, as tools for modulating or	
XX	CC	inhibiting the expression of genes and/or translation of transcripts, and	
XX	CC	as therapeutic agents. The proteins and peptides are useful as	
XX	CC	therapeutic, prognostic and diagnostic reagents for cancer. The present	
XX	CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example	
XX	CC	from the invention	
XX	SQ	Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 RKRRKR 6	
DB	DB	3 RKRRKR 8	
		Sequence 10 AA;	
		Query Match 100.0%; Score 30; DB 6; Length 10;	
		Best Local Similarity 100.0%; Pred. No. 86;	
		Matches 6;	

PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 200; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRKRK 6
 Db |||||
 3 RKRKRK 8
 RESULT 29
 ABR08212
 ID ABR08212 standard; peptide; 10 AA.
 XX
 AC ABR08212;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #747.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX

PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 194; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
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 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRKRK 6
 Db |||||
 2 RKRKRK 7
 RESULT 30
 ABR07803
 ID ABR07803 standard; peptide; 10 AA.
 XX
 AC ABR07803;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #338.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 190; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKRRKR 6
|||
Db 4 RKRRKR 9

Search completed: April 13, 2006, 08:45:09
Job time : 190 secs

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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:49:20 ; Search time 46 Seconds
(without alignments)
10.784 Million cell updates/sec

Title: US-09-816-688B-1
Perfect score: 30
Sequence: 1 KRKRK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RB COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	1 US-08-487-037-5	Sequence 5, Appl
2	30	100.0	9	1 US-08-332-518-10	Sequence 10, Appl
3	30	100.0	9	1 US-08-378-709-11	Sequence 11, Appl
4	30	100.0	21	1 US-07-678-974D-66	Sequence 66, Appl
5	30	100.0	21	1 US-08-945-168-72	Sequence 72, Appl
6	27	90.0	8	2 US-10-028-056-25	Sequence 25, Appl
7	27	90.0	9	1 US-08-332-518-2	Sequence 2, Appl
8	27	90.0	9	1 US-08-332-518-8	Sequence 8, Appl
9	27	90.0	9	1 US-08-332-518-9	Sequence 9, Appl
10	27	90.0	9	1 US-08-332-518-11	Sequence 11, Appl
11	27	90.0	9	1 US-08-378-709-3	Sequence 3, Appl
12	27	90.0	9	1 US-08-378-709-9	Sequence 9, Appl
13	27	90.0	9	1 US-08-378-709-10	Sequence 10, Appl
14	27	90.0	9	1 US-08-378-709-12	Sequence 12, Appl
15	27	90.0	11	4 PCT-US91-08328-15	Sequence 15, Appl
16	27	90.0	11	4 PCT-US91-08328-21	Sequence 21, Appl
17	27	90.0	12	1 US-08-378-709-31	Sequence 31, Appl
18	27	90.0	13	2 US-09-325-601-50	Sequence 50, Appl
19	26	86.7	13	2 US-09-325-601-37	Sequence 37, Appl
20	26	86.7	13	2 US-09-325-601-42	Sequence 42, Appl
21	26	86.7	13	2 US-09-325-601-46	Sequence 46, Appl
22	26	86.7	13	2 US-09-325-601-48	Sequence 48, Appl
23	25	83.3	5	1 US-08-595-043A-30	Sequence 30, Appl
24	25	83.3	6	2 US-09-351-414-7	Sequence 7, Appl
25	25	83.3	6	2 US-09-351-414-8	Sequence 8, Appl
26	25	83.3	8	1 US-08-249-387-6	Sequence 6, Appl
27	25	83.3	8	2 US-09-366-103-6	Sequence 6, Appl

28	83.3	11	4	PCT-US91-08328-17	Sequence 17, Appl
29	25	83.3	13	2 US-09-325-601-19	Sequence 19, Appl
30	25	83.3	13	2 US-09-325-601-28	Sequence 28, Appl
31	25	83.3	13	2 US-09-325-601-39	Sequence 39, Appl
32	25	83.3	13	2 US-09-325-601-44	Sequence 44, Appl
33	25	83.3	13	2 US-08-475-955-88	Sequence 88, Appl
34	25	83.3	13	2 US-07-867-819D-88	Sequence 88, Appl
35	24	80.0	6	1 US-07-906-930E-13	Sequence 13, Appl
36	24	80.0	6	1 US-08-332-518-20	Sequence 20, Appl
37	24	80.0	6	1 US-08-704-170-9	Sequence 9, Appl
38	24	80.0	6	1 US-08-487-046-4	Sequence 4, Appl
39	24	80.0	6	1 US-08-483-522-4	Sequence 4, Appl
40	24	80.0	6	2 US-09-083-259-5	Sequence 5, Appl
41	24	80.0	6	2 US-09-083-259-14	Sequence 14, Appl
42	24	80.0	6	2 US-09-396-195-5	Sequence 5, Appl
43	24	80.0	6	2 US-09-396-195-14	Sequence 14, Appl
44	24	80.0	6	2 US-09-648-400A-2	Sequence 2, Appl
45	24	80.0	6	2 US-09-792-480-2	Sequence 2, Appl
46	24	80.0	6	2 US-10-209-421-2	Sequence 2, Appl
47	24	80.0	6	2 US-09-801-676A-3	Sequence 3, Appl
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49	24	80.0	6	4 PCT-US94-02631-9	Sequence 9, Appl
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57	24	80.0	7	2 US-09-648-400A-6	Sequence 6, Appl
58	24	80.0	7	2 US-09-648-400A-24	Sequence 24, Appl
59	24	80.0	7	2 US-09-616-289-52	Sequence 52, Appl
60	24	80.0	7	2 US-09-792-480-3	Sequence 3, Appl
61	24	80.0	7	2 US-09-792-480-6	Sequence 6, Appl
62	24	80.0	7	2 US-09-792-480-25	Sequence 25, Appl
63	24	80.0	7	2 US-09-792-480-31	Sequence 31, Appl
64	24	80.0	7	2 US-09-792-480-32	Sequence 32, Appl
65	24	80.0	7	2 US-10-209-421-3	Sequence 3, Appl
66	24	80.0	7	2 US-10-209-421-6	Sequence 6, Appl
67	24	80.0	7	2 US-10-209-421-24	Sequence 24, Appl
68	24	80.0	7	2 US-10-209-421-37	Sequence 37, Appl
69	24	80.0	7	2 US-10-209-421-38	Sequence 38, Appl
70	24	80.0	7	2 US-10-144-549-7	Sequence 7, Appl
71	24	80.0	7	2 US-09-976-740-52	Sequence 52, Appl
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74	24	80.0	8	1 US-08-563-368B-2	Sequence 2, Appl
75	24	80.0	8	2 US-09-083-259-7	Sequence 7, Appl
76	24	80.0	8	2 US-09-083-259-16	Sequence 16, Appl
77	24	80.0	8	2 US-09-101-751A-2	Sequence 2, Appl
78	24	80.0	8	2 US-09-396-195-7	Sequence 7, Appl
79	24	80.0	8	2 US-09-396-195-16	Sequence 16, Appl
80	24	80.0	8	2 US-09-648-400A-4	Sequence 4, Appl
81	24	80.0	8	2 US-09-648-400A-25	Sequence 25, Appl
82	24	80.0	8	2 US-09-792-480-4	Sequence 4, Appl
83	24	80.0	8	2 US-09-792-480-26	Sequence 26, Appl
84	24	80.0	8	2 US-09-864-866-30	Sequence 30, Appl
85	24	80.0	8	2 US-10-209-421-41	Sequence 4, Appl
86	24	80.0	8	2 US-10-209-421-25	Sequence 25, Appl
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88	24	80.0	8	2 US-10-209-421-32	Sequence 32, Appl
89	24	80.0	8	2 US-10-209-421-33	Sequence 33, Appl
90	24	80.0	8	2 US-10-209-421-34	Sequence 34, Appl
91	24	80.0	8	2 US-10-209-421-35	Sequence 35, Appl
92	24	80.0	8	2 US-10-209-421-41	Sequence 41, Appl
93	24	80.0	8	2 US-10-209-421-44	Sequence 44, Appl
94	24	80.0	8	2 US-10-209-421-45	Sequence 45, Appl
95	24	80.0	8	2 US-09-999-724-2	Sequence 2, Appl
96	24	80.0	9	1 US-08-332-518-7	Sequence 7, Appl
97	24	80.0	9	1 US-08-332-518-12	Sequence 12, Appl
98	24	80.0	9	1 US-08-332-518-13	Sequence 13, Appl
99	24	80.0	9	1 US-08-332-518-17	Sequence 17, Appl
100	24	80.0	9	1 US-08-332-518-18	Sequence 18, Appl


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; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-332-518-10

Query Match 100.0%; Score 30; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 2 RKRRKR 7

RESULT 4
US-07-678-974D-66
; Sequence 66, Application US/07678974D
; Patent No. 5629146
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERMAN & AISENBERG
; STREET: 1730 RHODE ISLAND AVENUE, N.W.,
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-3186
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/678,974D
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AISENBERG, Irwin M.
; REGISTRATION NUMBER: 19,007
; REFERENCE/DOCKET NUMBER: SG19171
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-1404
; TELEFAX: 202-872-0493
; TELEX: 440 069 AIS UI
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-678-974D-66

Query Match 100.0%; Score 30; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 4 RKRRKR 9

RESULT 5
US-08-945-168-72
; Sequence 72, Application US/08945168
; Patent No. 5989548
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
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ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,168
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00533
FILING DATE: 23-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9501512-9
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-945-168-72

Query Match 100.0%; Score 30; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 4 RRRRR 9

RESULT 6
US-10-028-056-25
Sequence 25, Application US/10028056
Patent No. 6869766
GENERAL INFORMATION:
APPLICANT: PTERFY, MIKLOS
TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSY AND INSULIN
FILE REFERENCE: 407T-98010US
CURRENT APPLICATION NUMBER: US/10/028,056
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,772
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-028-056-25

Query Match 90.0%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 4 RRRRR 9

Db 1 KRRRR 6
RESULT 7
US-08-332-518-2
Sequence 2, Application US/08332518
Patent No. 5633230
GENERAL INFORMATION:
APPLICANT: TWIST, Michael
TITLE OF INVENTION: SUMMER-SMITH, Martin
TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,518
FILING DATE: 31-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,757
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,398
FILING DATE: 23-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,735
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,953
FILING DATE: 24-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,742
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,318
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/266/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-332-518-2

Query Match 90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 2 KRRRR 7

RESULT 8
US-08-332-518-8


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; Sequence 8, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-332-518-8

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Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 RKRKR 6

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RESULT 9
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; Sequence 9, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin

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; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-332-518-9

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Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RKRKR 6
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Db      2 RKRKR 7

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RESULT 10
US-08-332-518-11
; Sequence 11, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500

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/ FILING DATE: 23-OCT-1991
/ PRIOR APPLICATION DATA: US 07/602,953
/ APPLICATION NUMBER: US 07/602,953
/ FILING DATE: 24-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16777/176 ALLE
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-9
/
/ Query Match 90.0%; Score 27; DB 1; Length 9;
/ Best Local Similarity 83.3%; Pred. No. 4.6e+05;
/ Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 RKRRK 6
/ DB 1 RKRRR 6
/
/ RESULT 13
/ US-08-378-709-10
/ Sequence 10, Application US/08378709
/ Patent No. 5831001
/ GENERAL INFORMATION:
/ APPLICANT: TWIST, Michael
/ APPLICANT: BARNETT, Richard
/ APPLICANT: REID, Lorne
/ APPLICANT: SUMNER-SMITH, Martin
/ TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/378,709
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/872,398
/ FILING DATE: 23-APR-1992
/ APPLICATION NUMBER: US 07/779,735
/ FILING DATE: 23-OCT-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/602,953
/ FILING DATE: 24-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16777/176 ALLE
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-12
/
/ Query Match 90.0%; Score 27; DB 1; Length 9;
/ Best Local Similarity 83.3%; Pred. No. 4.6e+05;
/ Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 RKRRK 6
/ DB 1 RKRRR 6
/
/ RESULT 14
/ US-08-378-709-12
/ Sequence 12, Application US/08378709
/ Patent No. 5831001
/ GENERAL INFORMATION:
/ APPLICANT: TWIST, Michael
/ APPLICANT: BARNETT, Richard
/ APPLICANT: REID, Lorne
/ APPLICANT: SUMNER-SMITH, Martin
/ TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/378,709
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/872,398
/ FILING DATE: 23-APR-1992
/ APPLICATION NUMBER: US 07/779,735
/ FILING DATE: 23-OCT-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/602,953
/ FILING DATE: 24-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16777/176 ALLE
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-12
/
/ Query Match 90.0%; Score 27; DB 1; Length 9;
/ Best Local Similarity 83.3%; Pred. No. 4.6e+05;
/ Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 RKRRK 6
/ DB 2 RRRRR 7
/
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
```

RESULT 15
PCT-US91-08328-15
; Sequence 15, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 5..211
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg4-Glu-Arg-Ser-Arg-Gly-Asp-Val
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-15

Query Match 90.0%; Score 27; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

RESULT 16
PCT-US91-08328-21
; Sequence 21, Application PC/TUS9108328
; GENERAL INFORMATION:

; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 2..211
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg-Glu-Arg4-Ser-Arg-Gly-Asp-Val"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-21

Query Match 90.0%; Score 27; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
DB 1 RRRRR 6

RESULT 17
US-08-378-709-31
; Sequence 31, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne

APPLICANT: SUMNER-SMITH, Martin
TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,709
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,398
FILING DATE: 23-APR-1992
APPLICATION NUMBER: US 07/779,735
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,953
FILING DATE: 24-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/176 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-378-709-31

Query Match 90.0%; Score 27; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 4 KRRKRK 9

RESULT 18
US-09-325-601-50
Sequence 50, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-50

Query Match 90.0%; Score 27; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
DB 2 RKRRRR 7
RESULT 19
US-09-325-601-37
Sequence 37, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-37

Query Match 86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 2 RKQKRK 7

RESULT 20
US-09-325-601-42
Sequence 42, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-42

Query Match 86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 2 RKQKRK 7

RESULT 21
US-09-325-601-46

```
; Sequence 46, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-46

Query Match      86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRKRK 6
        |||||
DB      2 RKRKRQ 7

RESULT 22
US-09-325-601-48
; Sequence 48, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-48

Query Match      86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRKRK 6
        |||||
DB      2 RKRKRQ 7

RESULT 23
US-08-595-043A-30
; Sequence 30, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SCARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
```

```
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-595-043A-30

Query Match      83.3%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRKRK 5
        |||||
DB      1 RKRKRK 5

RESULT 24
US-09-351-414-7
; Sequence 7, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-351-414-7

Query Match      83.3%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RKRKRK 6
        |||||
DB      1 RKRKRK 5

RESULT 25
US-09-351-414-8
; Sequence 8, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
```

APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antigenic peptide
US-09-351-414-8

Query Match 83.3%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRKR 6
DB 2 KRKR 6

RESULT 26
US-08-249-387-6
Sequence 6, Application US/08249387
Patent No. 5681700
GENERAL INFORMATION:
APPLICANT: Reichlin, Morris
APPLICANT: Koren, Eugen
TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,387
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP145
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-249-387-6

Query Match 83.3%; Score 25; DB 1; Length 8;

APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antigenic peptide
US-09-351-414-8

Query Match 83.3%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRKR 6
DB 2 KRKR 6

RESULT 27
US-09-366-103-6
Sequence 6, Application US/09366103
Patent No. 6280944
GENERAL INFORMATION:
APPLICANT: Reichlin, Morris
APPLICANT: Koren, Eugen
TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA Antibodies
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street,
STREET: Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,103
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/450,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP145
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-09-366-103-6

Query Match 83.3%; Score 25; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KRKR 6
DB 2 KRKR 7

RESULT 28
PCT-US91-08328-17
Sequence 17, Application PC/TUS9108328
GENERAL INFORMATION:
APPLICANT: Ruggeri, Zaverio M.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING

```
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 4..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg3-Glu-Arg2-Ser-Arg-Gly-Asp-Val"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US Bi 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
; PCT-US91-08328-17

Query Match 83.3%; Score 25; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 6
DB 3 RKRRSR 8

RESULT 29
US-09-325-601-19
; Sequence 19, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

Search completed: April 13, 2006, 08:50:34
Job time : 47 secs

; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-19

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

RESULT 30
US-09-325-601-28
; Sequence 28, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-28

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

Search completed: April 13, 2006, 08:50:34
Job time : 47 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:50:49 ; Search time 26 Seconds
(without alignments)
9.805 Million cell updates/sec

Title: US-09-816-688b-1
Perfect score: 30
Sequence: 1 KRKRK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 76596

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications AA New:
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep:
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep:
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6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	90.0	8	US-10-512-299A-45	Sequence 45, Appl
2	26	86.7	10	US-10-918-638-1	Sequence 1, Appli
3	26	86.7	10	US-10-246-300D-1	Sequence 1, Appli
4	26	86.7	20	US-11-223-699A-66	Sequence 66, Appl
5	26	86.7	20	US-11-121-566A-66	Sequence 66, Appl
6	25	83.3	5	US-11-179-639-21	Sequence 21, Appl
7	25	83.3	6	US-11-242-243-7	Sequence 7, Appli
8	25	83.3	6	US-11-242-243-8	Sequence 8, Appli
9	25	83.3	21	US-10-512-299A-55	Sequence 55, Appl
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11	24	80.0	7	US-10-923-112A-44	Sequence 44, Appl
12	24	80.0	7	US-11-041-103-5	Sequence 5, Appli
13	24	80.0	7	US-11-107-371-6	Sequence 6, Appli
14	24	80.0	7	US-11-141-725-10	Sequence 10, Appl
15	24	80.0	7	US-11-223-699A-12	Sequence 12, Appl
16	24	80.0	7	US-11-223-699A-64	Sequence 64, Appl
17	24	80.0	7	US-11-121-566A-12	Sequence 12, Appl
18	24	80.0	7	US-11-121-566A-64	Sequence 64, Appl
19	24	80.0	8	US-11-019-894A-26	Sequence 26, Appl
20	24	80.0	8	US-11-155-845-2	Sequence 2, Appli
21	24	80.0	8	US-11-075-648A-8	Sequence 8, Appli
22	24	80.0	9	US-10-985-426-7	Sequence 7, Appli
23	24	80.0	9	US-10-509-787A-140	Sequence 140, App
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25	24	80.0	9	US-11-016-542-20	Sequence 20, Appl

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36	24	80.0	12	US-10-877-961B-91	Sequence 91, Appl
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38	24	80.0	12	US-10-913-711B-34	Sequence 34, Appl
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41	24	80.0	12	US-11-136-245A-16	Sequence 16, Appl
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43	24	80.0	12	US-11-133-804-49	Sequence 49, Appl
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45	24	80.0	12	US-11-133-804-80	Sequence 80, Appl
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47	24	80.0	13	US-11-019-894A-7	Sequence 7, Appli
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59	24	80.0	17	US-10-834-397-206	Sequence 206, App
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69	24	80.0	18	US-10-903-612B-102	Sequence 102, App
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74	24	80.0	19	US-10-903-612B-13	Sequence 13, Appl
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97	24	80.0	20	US-10-903-612B-49	Sequence 49, Appl
98	24	80.0	20	US-10-903-612B-85	Sequence 85, Appl

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118 24 80.0 21 7 US-11-081-140-3 Sequence 3, Appli
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120 23 76.7 9 6 US-10-523-038-43 Sequence 43, Appli
121 23 76.7 9 6 US-10-512-299A-20 Sequence 20, Appli
122 23 76.7 9 6 US-10-912-460-1 Sequence 1, Appli
123 23 76.7 9 7 US-11-178-868-1 Sequence 1, Appli
124 23 76.7 9 7 US-11-045-024-10434 Sequence 10434, A
125 23 76.7 9 7 US-11-045-024-12268 Sequence 12268, A
126 23 76.7 9 7 US-11-127-932-22 Sequence 22, Appli
127 23 76.7 9 7 US-11-016-542-2 Sequence 2, Appli
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129 23 76.7 9 7 US-11-127-903-50 Sequence 50, Appli
130 23 76.7 9 7 US-11-091-336-2 Sequence 2, Appli
131 23 76.7 9 7 US-11-141-725-7 Sequence 7, Appli
132 23 76.7 10 6 US-10-444-662-1 Sequence 1, Appli
133 23 76.7 10 7 US-11-032-794-53 Sequence 53, Appli
134 23 76.7 10 7 US-11-102-432-1 Sequence 1, Appli
135 23 76.7 10 7 US-11-119-098-8 Sequence 8, Appli
136 23 76.7 10 7 US-11-045-024-10432 Sequence 10432, A
137 23 76.7 10 7 US-11-045-024-12266 Sequence 12266, A
138 23 76.7 10 7 US-11-170-652-9 Sequence 9, Appli
139 23 76.7 11 6 US-10-444-662-7 Sequence 7, Appli
140 23 76.7 11 6 US-10-507-275-13 Sequence 13, Appli
141 23 76.7 11 6 US-10-839-966-2 Sequence 2, Appli
142 23 76.7 11 6 US-10-524-919-7 Sequence 7, Appli
143 23 76.7 11 6 US-10-508-504-2 Sequence 2, Appli
144 23 76.7 11 6 US-10-877-961B-252 Sequence 252, Appli
145 23 76.7 11 6 US-10-909-769-5 Sequence 5, Appli
146 23 76.7 11 6 US-10-923-112A-26 Sequence 26, Appli
147 23 76.7 11 6 US-10-517-710-24 Sequence 24, Appli
148 23 76.7 11 6 US-10-955-739-2 Sequence 2, Appli
149 23 76.7 11 7 US-11-111-463-7 Sequence 7, Appli
150 23 76.7 11 7 US-11-045-024-3499 Sequence 3499, Ap

ALIGNMENTS

RESULT 1
US-10-512-299A-45
; Sequence 45, Application US/10512299A
; Publication No. US20060057668A1
; GENERAL INFORMATION:
; APPLICANT: TOAGOSEI CO., LTD.
; APPLICANT: YOSHIDA, Tetsuhiko
; APPLICANT: KUME, Masayoshi
; APPLICANT: YAMADA, Yoshinao
; APPLICANT: KOURAI, Hiroki
; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
; FILE REFERENCE: 54003.8003.US00
; CURRENT APPLICATION NUMBER: US/10/512,299A
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/JP03/05225
; PRIOR FILING DATE: 2003-04-24

Query Match 90.0%; Score 27; DB 6; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.8e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRKR 6
Db 2 RRRRKR 7
|||:|

RESULT 2
US-10-918-638-1
; Sequence 1, Application US/10918638
; Publication No. US20050249663A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
; TITLE OF INVENTION: AND
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/918,638
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US/10/246,300
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TAT nuclear localization signal peptide
US-10-918-638-1

Query Match 86.7%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRKR 6
Db 3 RRRRKR 8
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RESULT 3
US-10-246-300D-1
; Sequence 1, Application US/10246300D
; Publication No. US20060074034A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS AND
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/246,300D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TAT nuclear localization signal peptide
US-10-246-300D-1

Query Match 86.7%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 4
US-11-223-699A-66
; Sequence 66, Application US/11223699A
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; TITLE OF INVENTION: RIBONUCLEIC ACID TO A CELL
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
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; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (19)
; OTHER INFORMATION: D-Gln
US-11-223-699A-66

Query Match 86.7%; Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 5
US-11-121-566A-66
; Sequence 66, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; FILE REFERENCE: 04-03US
; CURRENT APPLICATION NUMBER: US/11/121,566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
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; LOCATION: (17)
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; FEATURE:
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; LOCATION: (19)
; OTHER INFORMATION: D-Gln
US-11-121-566A-66

Query Match 86.7%; Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 6

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US-11-179-639-21
; Sequence 21, Application US/11179639
; Publication No. US20060034805A1
; GENERAL INFORMATION:
; APPLICANT: FANG, JIANMIN
; APPLICANT: JOOSS, KARIN
; TITLE OF INVENTION: AAV VECTOR COMPOSITIONS AND METHODS FOR ENHANCED
; FILE REFERENCE: 3802-101-11 US
; CURRENT APPLICATION NUMBER: US/11/179,639
; PRIOR FILING DATE: 2005-07-13
; PRIOR APPLICATION NUMBER: 60/587,082
; PRIOR FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 60/659,871
; PRIOR FILING DATE: 2005-03-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-179-639-21

Query Match      83.3%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 7
US-11-242-243-7
; Sequence 7, Application US/11242243
; Publication No. US20060024805A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/11/242,243
; PRIOR FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-11-242-243-7

Query Match      83.3%; Score 25; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 8
US-11-242-243-8
; Sequence 8, Application US/11242243
; Publication No. US20060024805A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/11/242,243
; PRIOR FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-11-242-243-8

Query Match      83.3%; Score 25; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 9
US-10-512-299A-55
; Sequence 55, Application US/10512299A
; Publication No. US20060057668A1
; GENERAL INFORMATION:
; APPLICANT: TOAGOSEI CO., LTD.
; APPLICANT: YOSHIDA, Tetsuhiko
; APPLICANT: KUME, Msayoshi
; APPLICANT: YAMADA, Yoshinao
; APPLICANT: KOURAI, Hiroki
; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
; FILE REFERENCE: 54003.8003.US00
; CURRENT APPLICATION NUMBER: US/10/512,299A
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/JP03/05225
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2002-124830
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 21
; TYPE: PPT
; ORGANISM: Rattus sp.
US-10-512-299A-55

Query Match      83.3%; Score 25; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRRK 5
DB 5 KRRRK 9

RESULT 10
US-10-850-207-8
; Sequence 8, Application US/10850207
; Publication No. US20050283003A1
; GENERAL INFORMATION:
; APPLICANT: Spudich, James A.
; APPLICANT: Nock, Steffen
; APPLICANT: Wagner, Peter
```

```
; TITLE OF INVENTION: Reversible Immobilization of Arginine-Tagged Moieties on a Silica
; FILE REFERENCE: UCSD-04726
; CURRENT APPLICATION NUMBER: US/10/850,207
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/486,480
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: PCT/US98/18531
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/057,929
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-850-207-8

Query Match      80.0%; Score 24; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 1 RRRRRR 6

RESULT 11
US-10-923-112A-44
; Sequence 44, Application US/10923112A
; Publication No. US20060040879A1
; GENERAL INFORMATION:
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 3293
; CURRENT APPLICATION NUMBER: US/10/923,112A
; CURRENT FILING DATE: 2004-08-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-923-112A-44

Query Match      80.0%; Score 24; DB 6; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 1 RRRRRR 6

RESULT 12
US-11-041-103-5
; Sequence 5, Application US/11041103
; Publication No. US20050287548A1
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; APPLICANT: Bao, Gang
; APPLICANT: Nitin, Nitin
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection
; FILE REFERENCE: 820701-1195
; CURRENT APPLICATION NUMBER: US/11/041,103
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: 10/179,730
; PRIOR FILING DATE: 2002-06-25
```

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; PRIOR APPLICATION NUMBER: 60/300,672
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/303,258
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
US-11-041-103-5
```

```
Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RKRRKR 6
Db 1 RRRRRR 6
```

```
RESULT 13
US-11-107-371-6
; Sequence 6, Application US/11107371
; Publication No. US20060014289A1
; GENERAL INFORMATION:
; APPLICANT: AHMADIAN, MOHAMMAD
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, LISHAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: DOUBLE-STRANDED RNA OR A DOUBLE-STRANDED HYBRID NUCLEIC
; TITLE OF INVENTION: ACID TO REGULATE GENE EXPRESSION IN MAMMALIAN CELLS
; FILE REFERENCE: 04-0205
; CURRENT APPLICATION NUMBER: US/11/107,371
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/564,543
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-107-371-6
```

```
Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RKRRKR 6
Db 1 RRRRRR 6
```

```
RESULT 14
US-11-141-725-10
; Sequence 10, Application US/11141725
; Publication No. US20060014712A1
; GENERAL INFORMATION:
; APPLICANT: Neuman, Thomas
; TITLE OF INVENTION: Controlled Delivery of Therapeutic Compounds
; FILE REFERENCE: 34211/US/2 (473322-00024)
```

```
; CURRENT APPLICATION NUMBER: US/11/141,725
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,660
; PRIOR FILING DATE: 2004-05-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-141-725-10

Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRRKR 6
Db      1 RRRRRR 6

RESULT 15
US-11-223-699A-12
; Sequence 12, Application US/11223699A
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: 11/121,566
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: BrAc-Arg
US-11-223-699A-64

Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRRKR 6
Db      1 RRRRRR 6

RESULT 17
US-11-121-566A-12
; Sequence 12, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; FILE REFERENCE: 04-03US
; CURRENT APPLICATION NUMBER: US/11/121,566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
```

; PRIOR APPLICATION NUMBER: 60/570,512
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/568,027
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 12
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-11-121-566A-12

Query Match 80.0%; Score 24; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 18
 US-11-121-566A-64
 ; Sequence 64, Application US/11121566A
 ; Publication No. US20060040882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, LISHAN
 ; APPLICANT: CUI, KUNYUAN
 ; APPLICANT: CHEN, YUCHING
 ; APPLICANT: MAYER, SASHA
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
 ; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
 ; TITLE OF INVENTION: OF TARGET GENES IN CELLS
 ; FILE REFERENCE: 04-03US
 ; CURRENT APPLICATION NUMBER: US/11/121,566A
 ; CURRENT FILING DATE: 2005-05-04
 ; PRIOR APPLICATION NUMBER: 60/667,833
 ; PRIOR FILING DATE: 2005-04-01
 ; PRIOR APPLICATION NUMBER: 60/656,572
 ; PRIOR FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: 60/613,416
 ; PRIOR FILING DATE: 2004-09-27
 ; PRIOR APPLICATION NUMBER: 60/570,513
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/570,512
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/568,027
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 64
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: BrAc-Arg
 US-11-121-566A-64

Query Match 80.0%; Score 24; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 19
 US-11-019-894A-26
 ; Sequence 26, Application US/11019894A
 ; Publication No. US20050245451A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pincus, Matthew R.
 ; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED
 ; TITLE OF INVENTION: MAMMALIAN CELLS
 ; FILE REFERENCE: 1181-17 CIP A
 ; CURRENT APPLICATION NUMBER: US/11/019,894A
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: 10/386,737
 ; PRIOR FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: 09/827,683
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,102
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/363,785
 ; PRIOR FILING DATE: 2002-03-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 26
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide; Arg(8) membrane penetrating leader sequence
 US-11-019-894A-26

Query Match 80.0%; Score 24; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 20
 US-11-155-845-2
 ; Sequence 2, Application US/11155845
 ; Publication No. US20050277193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WICKHAM, THOMAS J.
 ; APPLICANT: KOVESDI, IMRE
 ; APPLICANT: BROUGH, DOUGLAS E.
 ; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 ; FILE REFERENCE: 235922
 ; CURRENT APPLICATION NUMBER: US/11/155,845
 ; CURRENT FILING DATE: 2005-08-17
 ; PRIOR APPLICATION NUMBER: US 09/999,724
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 09/101,751
 ; PRIOR FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: PCT/US96/191500
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 08/700,846
 ; PRIOR FILING DATE: 1996-08-21
 ; PRIOR APPLICATION NUMBER: US 08/701,124
 ; PRIOR FILING DATE: 1996-08-21
 ; PRIOR APPLICATION NUMBER: US 08/563,368
 ; PRIOR FILING DATE: 1995-11-28
 ; NUMBER OF SEQ ID NOS: 94
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 2
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-11-155-845-2

Query Match 80.0%; Score 24; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 1 RRRRR 6

RESULT 21

US-11-075-648A-8
; Sequence 8, Application US/11075648A
; Publication No. US20060030535A1
; GENERAL INFORMATION:
; APPLICANT: Healy, Judith M.
; APPLICANT: Kurz, Markus
; APPLICANT: McCauley, Thomas Greene
; APPLICANT: Thompson, Kristin
; APPLICANT: Wilson, Charles
; APPLICANT: Margolskee, Dorothy J.
; TITLE OF INVENTION: Controlled Modulation of the Pharmacokinetics and Biodistribution
; FILE REFERENCE: 23239-575
; CURRENT APPLICATION NUMBER: US/11/075,648A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,790
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-075-648A-8

Query Match 80.0%; Score 24; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 1 RRRRR 6

RESULT 22

US-10-985-426-7
; Sequence 7, Application US/10985426
; Publication No. US20050256069A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: IRNA AGENTS WITH BIOCLEAVABLE TETHERS
; FILE REFERENCE: 14174-099001
; CURRENT APPLICATION NUMBER: US/10/985,426
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 10/916,185
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597

; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-985-426-7

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 1 RRRRR 6

RESULT 23

US-10-509-787A-140
; Sequence 140, Application US/10509787A
; Publication No. US20050287602A1
; GENERAL INFORMATION:
; APPLICANT: O'DOWD, BRIAN P.
; APPLICANT: GEORGE, SUSAN R.
; TITLE OF INVENTION: METHOD OF IDENTIFYING TRANSMEMBRANE PROTEIN-INTERACTING COMPOUNDS
; FILE REFERENCE: 3477-110
; CURRENT APPLICATION NUMBER: US/10/509,787A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: PCT/CA03/00542
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/442,556
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/422,891
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/387,570
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/379,419
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/371,704
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-509-787A-140

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
Db 2 KKKRR 7

RESULT 24

US-10-512-299A-12
; Sequence 12, Application US/10512299A
; Publication No. US20060057668A1
; GENERAL INFORMATION:
; APPLICANT: TOGOSSEI CO., LTD.

; APPLICANT: YOSHIDA, Tetsuhiko
; APPLICANT: KUME, Meayoshi
; APPLICANT: YAMADA, Yoshinao
; APPLICANT: KOURAI, Hiroki
; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
; FILE REFERENCE: 54003.8003.US00
; CURRENT APPLICATION NUMBER: US/10/512,299A
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/JP03/05225
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2002-124830
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-512-299A-12

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 2 KKRRKR 7

RESULT 25
US-11-016-542-20
; Sequence 20, Application US/11016542
; Publication No. US2005028239A1
; GENERAL INFORMATION:
; APPLICANT: ALLBRITTON, NANCY L.
; APPLICANT: SIMS, CHRISTOPHER E.
; APPLICANT: ROSSI, FRANCIS M.
; APPLICANT: SOUGHAYER, JOSEPH S.
; TITLE OF INVENTION: A CELL-PERMEABLE ENZYME ACTIVATION REPORTER THAT CAN BE
; TITLE OF INVENTION: LOADED IN A HIGH THROUGHPUT AND GENTLE MANNER
; FILE REFERENCE: CAL02-003-US
; CURRENT APPLICATION NUMBER: US/11/016,542
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/530,875
; PRIOR FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-016-542-20

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 26
US-11-133-804-47
; Sequence 47, Application US/11133804
; Publication No. US20060041105A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Tao
; APPLICANT: Olsen, Emilia S.
; APPLICANT: Whitney, Michael

; APPLICANT: Tsien, Roger Y.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable
; FILE REFERENCE: 02307E-161520US
; CURRENT APPLICATION NUMBER: US/11/133,804
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 10/699,562
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: portion of compound (f) of Figure 17, R9, Arg9,
; OTHER INFORMATION: peptide portion B, uptake sequence
US-11-133-804-47

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 27
US-11-200-703-7
; Sequence 7, Application US/11200703
; Publication No. US20060058266A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kesavan, Venkitesamy
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: CHEMICALLY MODIFIED OLIGONUCLEOTIDES
; FILE REFERENCE: 14174-089001
; CURRENT APPLICATION NUMBER: US/11/200,703
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/600,703
; PRIOR FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-11-200-703-7

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 28
US-11-133-804-85
; Sequence 85, Application US/11133804
; Publication No. US20060041105A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Tao
; APPLICANT: Olsen, Emilia S.
; APPLICANT: Whitney, Michael
; APPLICANT: Tsien, Roger Y.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable

```
; FILE REFERENCE: 02307E-161520US
; CURRENT APPLICATION NUMBER: US/11/133,804
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 10/699,562
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:basic portion B
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa = lysinamide attached through alpha and
; OTHER INFORMATION: epsilon nitrogen-bound cargo molecule
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = dodecaheptyl-arginine
US-11-133-804-85
```

```
Query Match      80.0%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred.No. 46;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RKRKRK 6
   |::|:|
Db 2 RRRRRR 7
```

RESULT 29

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US-10-535-780-3
; Sequence 3, Application US/10535780
; Publication No. US20060026718A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Stefan
; APPLICANT: Marillonnet, Sylvestre
; APPLICANT: Klimyuk, Victor
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: Method of Controlling Cellular Processes in Plants
; FILE REFERENCE: 049202/289227
; CURRENT APPLICATION NUMBER: US/10/535,780
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: PCT/EP03/13018
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: DE 102 54 166.3
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane Translocation Signal
US-10-535-780-3
```

```
Query Match      80.0%; Score 24; DB 6; Length 11;
Best Local Similarity 66.7%; Pred.No. 50;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RKRKRK 6
   |::|:|
Db 1 RRRRRR 6
```

RESULT 30

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US-10-955-739-6
; Sequence 6, Application US/10955739
; Publication No. US20060067925A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Labhasetwar, Vinod D.
; APPLICANT: Reddy, Maram K.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR INHIBITING REPERFUSION INJURY IN THE
; FILE OF INVENTION: BRAIN
; FILE REFERENCE: NE-0016
; CURRENT APPLICATION NUMBER: US/10/955,739
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide targeting moiety.
US-10-955-739-6
```

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Query Match      80.0%; Score 24; DB 6; Length 11;
Best Local Similarity 66.7%; Pred.No. 50;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RKRKRK 6
   |::|:|
Db 3 RRRRRR 8
```

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Search completed: April 13, 2006, 08:53:54
Job time : 27 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 08:45:30 ; Search time 38 Seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-09-816-688B-1
Perfect score: 30
Sequence: 1 RRRRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	25	83.3	21	2 I58423	arylhydrocarbon re
2	22	73.3	10	2 A42089	transcription fact
3	22	73.3	18	2 PS0387	platelet-derived g
4	22	73.3	21	2 PN0082	sperm chromatin pr
5	21	70.0	16	2 A28144	ribosomal protein
6	20	66.7	19	2 B39845	pyrB leader peptid
7	20	66.7	21	2 PS0146	histone H1 - sea u
8	20	66.7	21	2 JH0361	carassin - goldfis
9	18	60.0	16	2 A35552	caldesmon - turkey
10	17	56.7	13	2 E39778	lactose phosphotra
11	17	56.7	14	2 PL0040	glycogen phosphory
12	17	56.7	19	2 A33361	CAMP-regulated pho
13	17	56.7	20	2 I55663	MHC HLA-DR gamma c
14	17	56.7	21	2 S61306	probable nitrate r
15	16	53.3	8	2 I64832	Ca2+-transporting
16	16	53.3	9	2 S78762	ribosomal protein
17	16	53.3	10	2 PQ0785	NADH2 dehydrogenas
18	16	53.3	16	2 A27803	myosin light chain
19	16	53.3	16	2 S05703	homeotic protein c
20	16	53.3	18	2 S54270	GATA-2 protein - A
21	16	53.3	19	4 I54264	rhodopsin single b
22	16	53.3	20	2 S00315	photosystem I chai
23	16	53.3	20	2 S28405	lamin B receptor -
24	15	50.0	14	2 S58426	spermathecin AWN h
25	15	50.0	15	2 S36888	ribosomal protein
26	15	50.0	15	2 S36891	vesiculakinin 1 - e
27	15	50.0	17	1 A61339	translation elonga
28	15	50.0	18	2 S45373	monocyte chemotact
29	15	50.0	20	2 I67551	

30	14	46.7	9	2 PC7076	spectrin alpha cha
31	14	46.7	10	2 F41839	ribosomal protein
32	14	46.7	11	2 J00395	hypothetical prote
33	14	46.7	11	2 PH0913	T-cell receptor be
34	14	46.7	12	2 A40763	sucrose-6-phosphat
35	14	46.7	12	2 S29859	gene p10 protein -
36	14	46.7	13	2 JH0460	corticostatic pept
37	14	46.7	13	2 I51432	histone H4-1 precu
38	14	46.7	14	2 PC1215	homeotic protein E
39	14	46.7	15	2 C48401	ribosomal protein
40	14	46.7	15	2 PH0772	T-cell receptor be
41	14	46.7	15	2 S36889	ribosomal protein
42	14	46.7	15	2 A32971	heparin-binding le
43	14	46.7	16	2 G45681	orf 61.1 - phage T
44	14	46.7	17	2 S61451	hypothetical prote
45	14	46.7	18	2 A40256	interleukin-7 rece
46	14	46.7	18	2 A61220	epsilon receptor m
47	14	46.7	20	2 S17461	flavodoxin B - Azo
48	14	46.7	20	2 S68620	histone H4 - sea u
49	14	46.7	20	2 S78763	ribosomal protein
50	14	46.7	21	2 B35417	30K serine protein
51	13	43.3	10	2 S71948	matrix metalloprot
52	13	43.3	12	2 PH1605	Ig H chain V-D-J r
53	13	43.3	13	2 S78519	ribosomal protein
54	13	43.3	13	2 S12388	arga protein - Sal
55	13	43.3	13	2 S36887	ribosomal protein
56	13	43.3	14	2 S33803	chaperone, TCP1-re
57	13	43.3	14	2 JH0328	probrusin tetrade
58	13	43.3	15	2 I49407	placental calcium-
59	13	43.3	15	2 C41383	32K variable histo
60	13	43.3	15	2 A61247	urogenital tumor m
61	13	43.3	16	2 A45133	casein kinase II (
62	13	43.3	16	2 I52226	aldehyde dehydroge
63	13	43.3	16	2 C37290	homeotic protein G
64	13	43.3	18	2 S02175	acrosin (EC 3.4.21
65	13	43.3	18	2 S39153	translation elonga
66	13	43.3	18	2 B48408	21K high mobility
67	13	43.3	19	2 A38382	15K protein A - ra
68	13	43.3	19	2 A48408	21K high mobility
69	13	43.3	20	2 A60525	lysozyme (EC 3.2.1
70	13	43.3	20	2 B38382	15K protein B - ra
71	13	43.3	20	2 S11416	ribosomal protein
72	13	43.3	20	2 S32387	ribosomal protein
73	13	43.3	20	2 B53592	H+-exporting ATPas
74	13	43.3	21	2 PC4381	dehydrin 7.5K poly
75	12	40.0	4	2 I40870	phospholipase C (5
76	12	40.0	7	2 B33541	hypothetical prote
77	12	40.0	8	2 A39892	P element, P cytot
78	12	40.0	8	2 PT0323	Ig heavy chain CRD
79	12	40.0	10	2 I52645	gene B-50 protein
80	12	40.0	11	2 A26930	ermG leader peptid
81	12	40.0	12	1 LFECPE	pyrE leader peptid
82	12	40.0	13	2 A53608	neurotensin - guin
83	12	40.0	14	2 S23639	Ig kappa chain J s
84	12	40.0	14	2 A41589	25K elastin-bindin
85	12	40.0	14	2 PA0045	porin por1 - Arabi
86	12	40.0	15	2 A35417	28K serine protein
87	12	40.0	15	2 S29175	D-galactose-bindin
88	12	40.0	16	2 S30384	hypothetical prote
89	12	40.0	16	2 S78415	ribosomal protein
90	12	40.0	16	2 E37290	homeotic protein G
91	12	40.0	17	2 A34835	monoclonal nonspec
92	12	40.0	17	2 A27636	cycotoxin B - Clos
93	12	40.0	17	2 A38824	tachyplesin I - ho
94	12	40.0	17	2 JX0125	tachyplesin III -
95	12	40.0	17	2 C94063	hypothetical prote
96	12	40.0	18	2 S56715	hydroxymethylgluta
97	12	40.0	18	2 PH1621	Ig H chain V-D-J r
98	12	40.0	18	2 JU0124	polypheumisin I - A
99	12	40.0	18	2 JU0125	polypheumisin II -
100	12	40.0	19	2 PC1322	hypothetical prote
101	12	40.0	19	2 A49725	valine-tRNA ligase
102	12	40.0	19	2 A49725	

103 12 40.0 19 2 S16332 peroxidase (EC 1.1
104 12 40.0 19 2 PC1324 hypothetical prote
105 12 40.0 19 2 JX0124 tachyplesin I prec
106 12 40.0 20 2 B33290 histone H2B - huma
107 12 40.0 20 2 A42267 J-kappa recombinat
108 12 40.0 21 2 I51224 somatotropin - chi
109 12 40.0 21 2 S34298 Ig-binding protein
110 12 40.0 21 2 C31182 hypothetical 2.4k
111 12 40.0 21 2 PQ0789 NADH2 dehydrogenas
112 12 40.0 21 2 T03773 probable histone H
113 11 36.7 6 2 B33932 Ig mu chain D regi
114 11 36.7 8 2 S70727 iggf protein - Shi
115 11 36.7 8 2 B54823 olfactory receptor
116 11 36.7 8 2 B54823 olfactory receptor
117 11 36.7 10 2 A54810 beta-neoendorphin
118 11 36.7 10 2 D54823 olfactory receptor
119 11 36.7 10 2 C54823 olfactory receptor
120 11 36.7 11 2 B43669 hypothetical prote
121 11 36.7 12 2 S01222 translation elonga
122 11 36.7 12 2 D28551 hypothetical prote
123 11 36.7 12 2 S10626 lipovitellin - Afr
124 11 36.7 12 2 T4420 hypothetical prote
125 11 36.7 13 1 UNBO neurotensin - bovi
126 11 36.7 13 1 UNOPT neurotensin - brus
127 11 36.7 13 2 A28505 neurotensin [valid
128 11 36.7 13 2 A61067 neurotensin - comm
129 11 36.7 13 2 PH1595 Ig H chain V-D-J r
130 11 36.7 13 2 G83988 hypothetical prote
131 11 36.7 14 2 B34135 DNA-binding protei
132 11 36.7 14 2 PH1617 Ig H chain V-D-J r
133 11 36.7 14 2 PH0762 T-cell receptor be
134 11 36.7 14 2 A37789 heat shock cognate
135 11 36.7 14 2 S45655 cathepsin L (EC 3.
136 11 36.7 14 2 G61308 hemocyanin chain 3
137 11 36.7 14 2 S68095 calcium-binding pr
138 11 36.7 14 2 H83778 hypothetical prote
139 11 36.7 15 2 S7584 T cell receptor V-
140 11 36.7 15 2 S02381 probable membrane
141 11 36.7 15 2 A17340 ribonucleoside-dip
142 11 36.7 16 2 PH1475 T-cell receptor be
143 11 36.7 16 2 A47393 neuropeptide calla
144 11 36.7 16 2 D98854 conserved hypothet
145 11 36.7 18 2 C30309 histone H4 - Euplo
146 11 36.7 18 2 P02339 Ig heavy chain CDR
147 11 36.7 18 2 B41589 40K elastin-bindin
148 11 36.7 18 2 A42016 mammary-derived gr
149 11 36.7 18 2 A20923 light meromyosin -
150 11 36.7 19 2 A44854 L-2,4-diaminobuty

ALIGNMENTS

RESULT 1
158423
arylhydrocarbon receptor - mouse
C:Species: Mus sp. (mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58423
R;Minura, J.; Ema, M.; Sogawa, K.; Ikawa, S.; Fujii-Kuriyama, Y.
Pharmacogenetics 4, 349-354, 1994
A>Title: A complete structure of the mouse Ah receptor gene.
A:Reference number: I58423; MUID:95218835; PMID:7704041
A:Accession: I58423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: UNIPARC:UPI00000003C8; GB:S76844; NID:g913085; PIDN:AAB33978.1; PID:
A:Gene: Ah

Query Match 83.3%; Score 25; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KRRKR 5
Db 12 KRRKR 16

RESULT 2
A42089
transcription factor I-POU protein, alternative splice form - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42089
R;Treacy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.G.
Cell 68, 491-505, 1992
A>Title: Twin of I-POU: a two amino acid difference in the I-POU homeodomain distinguishes
A:Reference number: A42089; MUID:92154665; PMID:1346754
A:Accession: A42089
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <TRE>
A:Cross-references: UNIPROT:P24350; UNIPARC:UPI000016C02D; GB:S82271; NID:g945517; PID:g
C:Genetics:
A:Gene: FlyBase:I Pou
A:Cross-references: FlyBase:FBgn0004418

Query Match 73.3%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KRRKR 6
Db 3 KRRKR 7

RESULT 3
PS0387
platelet-derived growth factor chain A2 - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-Sep-1993
C:Accession: PS0387
R;Nakahara, K.; Nishimura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, S.
Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A>Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascul
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: PS0387
A:Molecule type: mRNA
A:Residues: 1-18 <NAK>
A:Cross-references: UNIPARC:UPI00001764FC
A>Note: this protein corresponds to the glioma type of human A chain
C:Superfamily: platelet-derived growth factor

Query Match 73.3%; Score 22; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KRRKR 6
Db 8 KRRKR 12

RESULT 4
PN0082
sperm chromatin protein I2-2 - Argentinian shortfin squid (fragment)
C:Species: Illex argentinus (Argentinian shortfin squid)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PN0082
R;Osadchuk, L.A.; Levina, N.B.; Telezhinskaya, I.N.; Khrapunov, S.N.; Berdyshev, G.D.; A
Bioorg. Khim. 16, 448-455, 1990
A>Title: Primary structure of main nuclear protein from headleg mollusk Illex argentinus
A:Reference number: PN0081; MUID:90329035; PMID:2375775
A:Accession: PN0082

A:Molecule type: protein
 A:Residues: 1-21 <OSA>
 A:Cross-references: UNIPROT:Q7M323; UNIPARC:UPI00001771FA
 A:Experimental source: sperm
 C:Superfamily: sperm histone
 C:Keywords: sperm

Query Match 73.3%; Score 22; DB 2; Length 21;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 :|||
 Db 2 RRRRSR 7

RESULT 5
 A28144
 ribosomal protein S27a - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C:Accession: A28144
 R:Redman, K.D.; Rechsteiner, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic p
 A:Reference number: A28144; MUID:88169619; PMID:2832412
 A:Accession: A28144
 A:Molecule type: protein
 A:Residues: 1-16 <RED>
 A:Cross-references: UNIPROT:Q97577; UNIPARC:UPI0000177161
 C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C:Keywords: protein biosynthesis

Query Match 70.0%; Score 21; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 5.8e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 :|||:
 Db 2 KRRKKK 7

RESULT 6
 B39845
 pyrB leader peptide - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Oct-2004
 C:Accession: B39845
 R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
 J. Biol. Chem. 266, 9113-9127, 1991
 A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrimi
 A:Reference number: A39845; MUID:91225016; PMID:1709162
 A:Accession: B39845
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-19 <QUL>
 A:Cross-references: UNIPARC:UPI000017A35C; GB:M59757

Query Match 66.7%; Score 20; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5
 :|||
 Db 2 KRRK 5

RESULT 7
 PS0146
 histone H1 - sea urchin (Hemicentrotus pulcherrimus) (fragment)
 C:Species: Hemicentrotus pulcherrimus
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C:Accession: PS0146

R:Suzuki, M.; Sugiura, M.; Ebashi, S.
 J. Biochem. 108, 347-355, 1990
 A:Title: Sea urchin protease specific to the SPKK motif in histone.
 A:Reference number: PS0145; MUID:9115778; PMID:2126010
 A:Accession: PS0146
 A:Molecule type: protein
 A:Residues: 1-21 <SUZ>
 A:Cross-references: UNIPROT:Q7M3M1; UNIPARC:UPI000017BF14
 C:Keywords: chromosomal protein; nucleosome

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
 :|||
 Db 13 RSRRK 17

RESULT 8
 JH0361
 carassin - goldfish
 N:Alternate names: tachykinin-related peptide
 C:Species: Carassius auratus (goldfish)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
 C:Accession: JH0361
 R:Conlon, J.M.; O'Harte, P.; Peter, R.E.; Kah, O.
 J. Neurochem. 56, 1432-1436, 1991
 A:Title: Carassin: a tachykinin that is structurally related to neuropeptide-gamma from t
 A:Reference number: JH0361; MUID:91162221; PMID:2002352
 A:Accession: JH0361
 A:Molecule type: protein
 A:Residues: 1-21 <CON>
 A:Cross-references: UNIPROT:P25421; UNIPARC:UPI0000136FDE
 A:Experimental source: brain
 C:Keywords: amidated carboxyl end
 F:21/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
 :|||
 Db 9 RKRRK 13

RESULT 9
 A35552
 caldesmon - turkey (fragment)
 C:Species: Meleagris gallopavo (common turkey)
 C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 C:Accession: A35552
 R:Velaz, L.; Ingraham, R.H.; Chalovich, J.M.
 J. Biol. Chem. 265, 2929-2934, 1990
 A:Title: Dissociation of the effect of caldesmon on the ATPase activity and on the bindin
 A:Reference number: A35552; MUID:90153926; PMID:2137453
 A:Accession: A35552
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <VEL>
 A:Cross-references: UNIPROT:Q7LZ12; UNIPARC:UPI000017C045

Query Match 60.0%; Score 18; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
 :|||
 Db 10 RRQKR 14

RESULT 10

E39778
lactose phosphotransferase system lacR protein - Lactococcus lactis (fragment)
C:Species: Lactococcus lactis
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C:Accession: E39778
R:van Rooijen, R.J.; van Schalkwijk, S.; de Vos, W.M.
J. Biol. Chem. 266, 7176-7181, 1991
A:Title: Molecular cloning, characterization, and nucleotide sequence of the tagatose 6-phosphatase gene from *Lactococcus lactis*
A:Reference number: A39778; MUID:91201377; PMID:1901863
A:Accession: E39778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <VAN>
A:Cross-references: UNIPROT:P18916; UNIPARC:UPI00001787DC; GB:J05748
A:Superfamily: regulatory protein gutr
C:Keywords: DNA binding; transcription regulation

Query Match 56.7%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRK 4
Db 9 KRR 12

RESULT 11
PI0040
glycogen phosphorylase (EC 2.4.1.1), cardiac - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: PI0040
R:Dombradi, V.; Willis, A.C.; Vereb, G.; Johnson, L.N.
Comp. Biochem. Physiol. B 91, 717-721, 1988
A:Title: The sequence around the phosphorylation site of the porcine heart type phosphatase
A:Reference number: PI0040; MUID:89136523; PMID:3224509
A:Accession: PI0040
A:Molecule type: protein
A:Residues: 1-14 <DOM>
A:Cross-references: UNIPROT:Q7M385; UNIPARC:UPI000017C45F
A:Experimental source: heart
C:Keywords: allosteric regulation; cardiac muscle; glycogen metabolism; glycosyltransferase
F10/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 56.7%; Score 17; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRK 6
Db 4 ERKQ 8

RESULT 12
A3361
cAMP-regulated phosphoprotein, 21K - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
C:Accession: A3361
R:Hemmings Jr., H.C.; Girault, J.A.; Williams, K.R.; LoPresti, M.B.; Greengard, P.
J. Biol. Chem. 264, 7726-7733, 1989
A:Title: ARPP-21, a cyclic AMP-regulated phosphoprotein (M-r=21,000) enriched in dopaminergic studies of its phosphorylation in vitro.
A:Reference number: A3361; MUID:89214228; PMID:2540203
A:Accession: A3361
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <HEM>
A:Cross-references: UNIPROT:Q7M049; UNIPARC:UPI000017C8D7
C:Keywords: phosphoprotein

Query Match 56.7%; Score 17; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRK 5
Db 5 QERRK 9

RESULT 13
I5563
MHC HLA-DR gamma chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I5563
R:O'Sullivan, D.M.; Noonan, D.; Quaranta, V.
J. Exp. Med. 166, 444-460, 1987
A:Title: Four Ia invariant chain forms derive from a single gene by alternate splicing at the 5' end
A:Reference number: I5563; MUID:87252940; PMID:3036998
A:Accession: I5563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-20 <RES>
A:Cross-references: UNIPROT:O19685; UNIPARC:UPI00000895C2; GB:M28588; NID:G292150; PIDN:1
C:Genetics:
A:Gene: HLA-DR

Query Match 56.7%; Score 17; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRRK 6
Db 3 RRRSR 7

RESULT 14
S61306
probable nitrate reductase alpha chain - Thiosphaera pantotropha (fragment)
C:Species: Thiosphaera pantotropha
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: S61306
R:Berk, B.C.; Page, M.D.; Richardson, D.J.; Reilly, A.; Cavill, A.; Outen, F.; Ferguson, M.L. Microbiol. 15, 319-331, 1995
A:Title: Sequence analysis of subunits of the membrane-bound nitrate reductase from a denitrifying bacterium
A:Reference number: S61306; MUID:95264918; PMID:7746153
A:Accession: S61306
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-21 <BER>
A:Cross-references: UNIPARC:UPI00000B21EE; EMBL:Z26255; NID:G541760; PIDN:CAA81214.1; PII
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994
C:Genetics:
A:Gene: narG
C:Keywords: membrane-associated complex

Query Match 56.7%; Score 17; DB 2; Length 21;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRK 5
Db 15 KRRR 18

RESULT 15
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I64832
R:Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in

A:Reference number: I51892
A:Accession: I64832
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q63139; UNIPARC:UPI00001708F8; GB:M99223; NID:G203644; PIDN:
C:Genetics:
A:Gene: SBRCA1b
C:Keywords: hydrolase

Query Match 53.3%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5
:|:|:
DB 5 ERK 8

RESULT 16
S78762
Ribosomal protein MRP-S12, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: S78762
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760
A:Accession: S78762
A:Molecule type: protein
A:Residues: 1-9 <GRA>
A:Cross-references: UNIPROT:Q7M375; UNIPARC:UPI000017C56E
C:Keywords: mitochondrial
F:1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match 53.3%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:
DB 3 RKVRPR 8

RESULT 17
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 27K chain; NADH-ubiquinone reductase 27K chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: PQ0785
R:Letierme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993

A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:
A:Reference number: PQ0775; MUID:94151437; PMID:8108509
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
A:Cross-references: UNIPROT:Q7M2G2; UNIPARC:UPI000017CDA9
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th
ranging from 5K to 75K.

C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 53.3%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
:|:|:
DB 6 QKERK 10

RESULT 18

A27803
myosin light chain, smooth muscle - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: A27803
R:Bengur, A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.
J. Biol. Chem. 262, 7613-7617, 1987

A:Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle my
A:Reference number: A27803; MUID:87222380; PMID:3584131
A:Accession: A27803
A:Molecule type: protein
A:Residues: 1-16 <BEN>
A:Cross-references: UNIPROT:Q7LZ79; UNIPARC:UPI00001776E1
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand; muscle; smooth muscle

Query Match 53.3%; Score 16; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:
DB 11 KKRPR 16

RESULT 19

S05703
homeotic protein ceh-2 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004
C:Accession: S05703
R:Buerklin, T.R.; Finney, M.; Coulson, A.; Ruvkun, G.
Nature 341, 239-243, 1989

A:Title: Caenorhabditis elegans has scores of homeobox-containing genes.
A:Reference number: S05703; MUID:89384901; PMID:2571091
A:Accession: S05703
A:Status: not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 1-16 <BUE>
A:Cross-references: UNIPROT:O01962; UNIPARC:UPI000017A2EF
C:Genetics:
A:Gene: ceh-2
A:Map position: 1

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 53.3%; Score 16; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:
DB 9 RTKHKR 14

RESULT 20

SS4270
GATA-2 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: SS4270
R:Brewer, A.C.; Guille, M.J.; Fear, D.J.; Partington, G.A.; Patient, R.K.

EMBO J. 14, 757-766, 1995
A:Title: Nuclear translocation of a maternal CCAAT factor at the start of gastrulation a
A:Reference number: SS4270; MUID:95188880; PMID:7882979
A:Accession: SS4270
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-18 <BRE>
A:Cross-references: UNIPROT:Q7LZS3; UNIPARC:UPI000017BF91

Query Match 53.3%; Score 16; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRK 4
|:|
Db 9 RRR 12

RESULT 21
I54264
rhodopsin single base deletion frame shift mutant - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 20-Apr-2000
C:Accession: I54264
R:Horn, M.; Humphries, P.; Kunisch, M.; Marchese, C.; Apfelstedt-Sylla, E.; Fugl, L.; Z
Hum. Genet. 90: 255-257, 1992
A:Title: Deletions in exon 5 of the human rhodopsin gene causing a shift in the reading
A:Reference number: I54264; MUID:93138610; PMID:1487240
A:Accession: I54264
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <HOR>
A:Cross-references: UNIPARC:UPI000011DDF9; GB:S55843; NID:g266287; PIDN:AAB25673.1; PID:
C:Genetics:
A:Gene: GDB:RHO
A:Cross-references: GDB:120347
A:Map position: 3q21.3-3q24

Query Match 53.3%; Score 16; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRRKR 6
|:|
Db 1 RRRAR 5

RESULT 22
S00315
photosystem I chain III - garden pea (fragment)
N:Alternate names: photosystem I 17K chain
C:Species: Pisum sativum (garden pea)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00315; PT0018
R:Dunn, P.P.J.; Packman, L.C.; Pappin, D.; Gray, J.C.
PDB Lett. 228: 157-161, 1988
A:Title: N-terminal amino acid sequence analysis of the subunits of pea photosystem I.
A:Reference number: S00314; MUID:88137587; PMID:3277857
A:Accession: S00315
A:Molecule type: protein
A:Residues: 1-20 <DUN>
A:Cross-references: UNIPROT:P20119; UNIPARC:UPI0000132517
A>Note: 1-Ap was also found
C:Superfamily: photosystem I chain III
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 53.3%; Score 16; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRRKR 6
|:|
Db 16 KREKQ 20

RESULT 23
S28405
lamin B receptor - turkey (fragment)
N:Alternate names: inner nuclear membrane protein p58
C:Species: Meleagris gallopavo (common turkey)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28405

R:Simos, G.; Georgatos, S.D.
EMBO J. 11, 4027-4036, 1992
A:Title: The inner nuclear membrane protein p58 associates in vivo with a p58 kinase and
A:Reference number: S28405; MUID:93010998; PMID:1327755
A:Accession: S28405
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SIM>
A:Cross-references: UNIPROT:Q7LZ11; UNIPARC:UPI000017C046
C:Keywords: DNA binding; nucleus; receptor; transmembrane protein

Query Match 53.3%; Score 16; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5
|:|
Db 1 KQRK 4

RESULT 24
S58426
spermadhesin AWN homolog - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 12-Feb-1998 #sequence_revision 15-May-1998 #text_change 07-May-1999
C:Accession: S58426
R:Calvete, J.J.; Mann, K.; Schaefer, W.; Sanz, L.; Reinert, M.; Nessau, S.; Raida, M.; T
Biochem. J. 310, 615-622, 1995
A:Title: Amino acid sequence of HSP-1, a major protein of stallion seminal plasma: effect
A:Reference number: S58424; MUID:95382782; PMID:7654203
A:Accession: S58426
A:Molecule type: protein
A:Residues: 1-14 <CAL>
A:Cross-references: UNIPARC:UPI000017C44B
A:Experimental source: seminal plasma

Query Match 50.0%; Score 15; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RRRK 6
|:|
Db 4 RRR 7

RESULT 25
S36888
ribosomal protein S12 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36888
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
PDB Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36888
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
A:Cross-references: UNIPROT:Q53538; UNIPARC:UPI000017729F
C:Superfamily: ribosomal protein S12
C:Keywords: protein biosynthesis; ribosome

Query Match 50.0%; Score 15; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KRRRK 5
|:|
Db 8 RKGR 12

RESULT 26

S36891
ribosomal protein - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36891
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36891
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OH>
A:CROSS-references: UNIPROT:Q9R545; UNIPARC:UPI00000BDC05

Query Match 50.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RRR 5
| | |
Db 10 RRR 12

RESULT 27
A61339
vesiculakinin 1 - eastern yellowjacket
N:Contains: vesiculakinin 2
C:Species: Vespula maculifrons (eastern yellowjacket)
C:Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61339
R:Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A:Title: Vesiculakinins: new carbohydrate-containing bradykinin derivatives.
A:Reference number: A61339; MUID:76114777; PMID:1247511
A:Accession: A61339
A:Molecule type: protein
A:Residues: 1-17 <YOS>
A:CROSS-references: UNIPROT:P57672; UNIPARC:UPI0000138459
C:Superfamily: vesiculakinin
C:Keywords: antihypertensive; bradykinin; glycoprotein; venom
F:1-17/Product: vesiculakinin 1 #status experimental <MAT1>
F:3-17/Product: vesiculakinin 2 #status experimental <MAT2>
F:9-17/Region: bradykinin-like
F:3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 50.0%; Score 15; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRRKR 6
| | |
Db 5 RRRGR 9

RESULT 28
S45373
translation elongation factor EF-1a - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S45373
R:Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A:Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A:Reference number: S45372; MUID:94035181; PMID:8220482
A:Accession: S45373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <MAR>
A:CROSS-references: UNIPROT:Q40499; UNIPARC:UPI00000A6737; EMBL:Z14080; NID:G443955; PID:G443955

Query Match 50.0%; Score 15; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 5
| | |
Db 14 QRRKK 18

RESULT 29
I67551
monocyte chemotactic protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I67551
R:Steinberger, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Wester
Eur. J. Immunol. 24, 900-908, 1994
A:Title: B precursor acute lymphoblastic leukemia third complementarity-determining region
fecal life.
A:Reference number: I53401; MUID:94200227; PMID:8149961
A:Accession: I67551
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:CROSS-references: UNIPARC:UPI0000116D84; GB:S69743; NID:G546304; PID:G546304
C:Genetics:
A:Gene: Igh VDJ

Query Match 50.0%; Score 15; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRKR 5
| | |
Db 2 RRRDK 6

RESULT 30
PC7076
spectrin alpha chain, non-erythroid - mouse (fragment)
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: PC7076
R:Taugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; N
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:CROSS-references: UNIPROT:P16546; UNIPARC:UPI000017C74E
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C:Keywords: brain

Query Match 46.7%; Score 14; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 4
| | |
Db 5 RRRKK 8

Search completed: April 13, 2006, 08:49:44
Job time : 41 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:42:09 ; Search time 227 seconds
(without alignments)
18.648 Million cell updates/sec

Title: US-09-816-688B-1

Perfect score: 30

Sequence: 1 RRRKR 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	83.3	21	2	Q6LD79_MOUSE
2	25	83.3	21	2	Q6LEC9_MOUSE
3	22	73.3	16	2	Q9UD21_HUMAN
4	22	73.3	20	2	Q9DEH9_XENLA
5	22	73.3	21	2	Q7M3Z3_ILIAR
6	21	70.0	15	2	Q5RF91_PONPY
7	21	70.0	15	2	Q35411_MOUSE
8	21	70.0	17	2	Q76N52_HUMAN
9	21	70.0	19	2	Q9UDB7_HUMAN
10	21	70.0	19	2	Q8T0Y5_APIME
11	21	70.0	20	2	Q4ZG97_9DELA
12	21	70.0	20	2	Q4ZGB1_9DELA
13	21	70.0	20	2	Q4ZGB2_9DELA
14	21	70.0	21	2	Q9UC26_HUMAN
15	21	70.0	21	2	Q9UG23_9VIRU
16	21	70.0	21	2	Q9JG26_9VIRU
17	21	70.0	21	2	Q9JG30_9VIRU
18	20	66.7	10	2	Q8VN85_HELPY
19	20	66.7	14	2	Q4CX76_9CUCU
20	20	66.7	19	2	Q8HYW9_BOVIN
21	20	66.7	19	2	Q8Y922_BRARE
22	20	66.7	19	2	Q65MTO_9HIV1
23	20	66.7	20	2	Q4YAE2_PLABE
24	20	66.7	21	1	TKNC_CARAU
25	20	66.7	21	2	Q7M3M1_HEMPU
26	20	66.7	21	2	Q662J7_BORGA
27	20	66.7	21	2	Q9DD39_NIPNI
28	20	66.7	21	2	Q9PRZ3_ONCMY
29	19	63.3	20	2	Q70Y78_9LAMI
30	19	63.3	11	2	Q70Y85_9LAMI
31	19	63.3	13	2	Q65331_NPVAC

32	19	63.3	14	2	Q70Y82_9LAMI	Q70Y82 plectranthu
33	19	63.3	15	2	Q5XPT1_SOLITU	Q5XPT1 solanum tub
34	19	63.3	15	2	Q5PX33_9CHLO	Q5PX33 halimeda tu
35	19	63.3	15	2	Q7WR21_9FLAO	Q7WR21 flavobacter
36	19	63.3	17	2	Q5PX35_9CHLO	Q5PX35 halimeda tu
37	19	63.3	18	2	Q16173_HUMAN	Q16173 homo sapien
38	19	63.3	19	2	Q9UH46_HUMAN	Q9UH46 homo sapien
39	19	63.3	19	2	Q70Y86_9LAMI	Q70Y86 platostoma
40	19	63.3	20	2	Q7S325_NEUCR	Q7S325 neurospora
41	19	63.3	20	2	Q6UQN2_9PASE	Q6UQN2 anomalospi
42	19	63.3	20	2	Q6UQN3_9PASS	Q6UQN3 vidua orien
43	19	63.3	20	2	Q6UQN4_9PASS	Q6UQN4 vidua parad
44	19	63.3	20	2	Q6UQN5_9PASS	Q6UQN5 vidua obtus
45	19	63.3	20	2	Q6UQN6_9PASS	Q6UQN6 vidua hypoc
46	19	63.3	20	2	Q6UQN8_9PASS	Q6UQN8 vidua macro
47	19	63.3	20	2	Q6UQN9_9PASS	Q6UQN9 vidua wilso
48	19	63.3	20	2	Q6UQP0_9PASS	Q6UQP0 vidua camer
49	19	63.3	20	2	Q6UQP2_9PASS	Q6UQP2 vidua rari
50	19	63.3	20	2	Q6UQP3_9PASS	Q6UQP3 vidua purpu
51	19	63.3	20	2	Q6UQP4_9PASS	Q6UQP4 vidua regia
52	19	63.3	20	2	Q6UQP5_9PASS	Q6UQP5 vidua fisch
53	19	63.3	21	2	Q4XNU6_PLACH	Q4XNU6 plasmodium
54	18	60.0	11	2	Q8R2J7_MESAU	Q8R2J7 mesocricetu
55	18	60.0	13	2	Q9R8R9_STRPY	Q9R8R9 streptococc
56	18	60.0	15	2	Q6LC05_PSEAE	Q6LC05 pseudomonas
57	18	60.0	16	2	Q7LZ12_MELGA	Q7LZ12 meleagris g
58	18	60.0	17	2	Q79167_HORSE	Q79167 equus cabal
59	18	60.0	17	2	Q5KC74_EUGGL	Q5KC74 eucalyptus
60	18	60.0	18	2	Q7RNN4_PLAYO	Q7RNN4 plasmodium
61	18	60.0	19	2	Q4XDU3_PLACH	Q4XDU3 plasmodium
62	18	60.0	19	2	Q4Y054_PLACH	Q4Y054 plasmodium
63	18	60.0	19	2	Q4Y6H4_PLACH	Q4Y6H4 plasmodium
64	18	60.0	19	2	Q905G8_9HIV1	Q905G8 human immun
65	18	60.0	19	2	Q905I8_9HIV1	Q905I8 human immun
66	18	60.0	19	2	Q905J6_9HIV1	Q905J6 human immun
67	18	60.0	19	2	Q90RF8_9HIV1	Q90RF8 human immun
68	18	60.0	20	2	Q9UCM1_HUMAN	Q9UCM1 homo sapien
69	18	60.0	20	2	Q7RKX5_PLAYO	Q7RKX5 plasmodium
70	17	56.7	7	2	P92210_AGRCR	P92210 agropyron c
71	17	56.7	7	2	P92214_9FOAL	P92214 amblyopyrum
72	17	56.7	7	2	P92218_9FOAL	P92218 australopyr
73	17	56.7	7	2	P92221_BROIN	P92221 bromus iner
74	17	56.7	7	2	P92226_CRIDE	P92226 crithopsis
75	17	56.7	7	2	P92372_9FOAL	P92372 haynaldia v
76	17	56.7	7	2	P92381_9FOAL	P92381 hordeum bra
77	17	56.7	7	2	P92385_HORMA	P92385 hordeum mar
78	17	56.7	7	2	P92387_9FOAL	P92387 henrardia p
79	17	56.7	7	2	P92390_HETPI	P92390 heteranthel
80	17	56.7	7	2	P92393_HORVI	P92393 hordeum vul
81	17	56.7	7	2	P92403_LOPEL	P92403 lophopyrum
82	17	56.7	7	2	P92421_PSAFR	P92421 psathyrosta
83	17	56.7	7	2	P92425_PSEPI	P92425 pseudoroegn
84	17	56.7	7	2	P92427_9FOAL	P92427 peridictyon
85	17	56.7	7	2	P92430_ARGTA	P92430 aegilops ta
86	17	56.7	7	2	P92440_THIBE	P92440 thimopyrum
87	17	56.7	7	2	P92442_TARCM	P92442 taeniathecu
88	17	56.7	7	2	Q9YIQ3_ADE04	Q9YIQ3 human adeno
89	17	56.7	7	2	Q9YIY3_ADE07	Q9YIY3 human adeno
90	17	56.7	7	2	Q9YIY3_ADE07	Q9YIY3 human adeno
91	17	56.7	8	2	Q84271_HPV19	Q84271 human papil
92	17	56.7	8	2	Q84273_HPV25	Q84273 human papil
93	17	56.7	9	2	Q45852_CLOBU	Q45852 clostridium
94	17	56.7	12	2	Q5EFZ2_9BRYO	Q5EFZ2 buxbaumia a
95	17	56.7	13	2	Q9UM89_HUMAN	Q9UM89 homo sapien
96	17	56.7	13	2	Q60F86_9BRYO	Q60F86 sphagnum gi
97	17	56.7	13	2	Q60F89_TAKLE	Q60F89 takakia lep
98	17	56.7	14	2	Q7S9F5_NEUCR	Q7S9F5 neurospora
99	17	56.7	14	2	Q7M385_PIG	Q7M385 sus scrofa
100	17	56.7	15	2	Q15344_HUMAN	Q15344 homo sapien
101	17	56.7	16	2	Q9UD45_HUMAN	Q9UD45 homo sapien
102	17	56.7	16	2	Q9UD47_HUMAN	Q9UD47 homo sapien
103	17	56.7	18	2	Q5RL96_HUMAN	Q5RL96 homo sapien
104	17	56.7	18	2	Q4YAA7_PLABE	Q4YAA7 plasmodium

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105 17 56.7 18 2 QSEFY3 9BRYO Q5efy3 polytrichum
106 17 56.7 18 2 QSEFY6 9BRYO Q5efy6 andreaea ru
107 17 56.7 19 2 Q4YGN5 PLABE Q4ygn5 plasmodium
108 17 56.7 19 2 Q63058 LATCL Q63058 lathraea cl
109 17 56.7 19 2 Q7M049 RAT Q7m049 rattus norv
110 17 56.7 19 2 Q905E0 9HIV1 Q905e0 human immun
111 17 56.7 19 2 Q905I0 9HIV1 Q905i0 human immun
112 17 56.7 20 2 O19685 HUMAN O19685 homo sapien
113 17 56.7 20 2 Q4XJC5 PLACH Q4xjc5 plasmodium
114 17 56.7 20 2 Q4XJG0 PLACH Q4xjg0 plasmodium
115 17 56.7 20 2 Q4YX59 PLABE Q4yx59 plasmodium
116 17 56.7 21 1 ACLP MOUSE P81855 mus musculu
117 17 56.7 21 1 M1SG_MISAN P81474 miegurnus a
118 17 56.7 21 2 Q25084 HERMO Q25084 herdmania m
119 17 56.7 21 2 Q25087 HERMO Q25087 herdmania m
120 17 56.7 21 2 Q4YLQ4 PLABE Q4ylq4 plasmodium
121 17 56.7 21 2 QSEFY9 9BRYO Q5efy9 oedipodium
122 17 56.7 21 2 QSEG70 9BRYO Q5eg70 sphagnum fi
123 17 56.7 21 2 Q56354 PARDE Q56354 paracoccus
124 16 53.3 8 2 Q7BED1 RAT Q7bed1 rattus norv
125 16 53.3 9 2 Q6KERO HUMAN Q6ker0 homo sapien
126 16 53.3 9 2 Q6LDS7 RABIT Q6lds7 oryctolagus
127 16 53.3 9 2 Q7M375 BOVIN Q7m375 bos taurus
128 16 53.3 9 2 Q9T777 BOVIN Q9t777 bos taurus
129 16 53.3 9 2 Q85V64 EUGR Q85v64 eucalyptus
130 16 53.3 9 2 Q93E20 STRAG Q93e20 streptococc
131 16 53.3 9 2 Q69349 HHV2 Q69349 human herpe
132 16 53.3 10 2 Q7M2G2 VICFA Q7m2g2 vicia faba
133 16 53.3 10 2 Q85BV6 EUGR Q85bv6 eucalyptus
134 16 53.3 10 2 Q85BV7 EUGR Q85bv7 eucalyptus
135 16 53.3 12 2 Q9P116 HUMAN Q9p116 homo sapien
136 16 53.3 13 2 Q9UJ52 HUMAN Q9uj52 homo sapien
137 16 53.3 13 2 Q80Y02 9MURI Q80y02 rattus sp.
138 16 53.3 14 2 Q56LZ6 DROME Q56l26 drosophila
139 16 53.3 14 2 P71199 ECOLI P71199 escherichia
140 16 53.3 14 2 Q9CW75 9MURI Q9cw75 mus sp. hom
141 16 53.3 15 2 Q86WB2 HUMAN Q86wb2 homo sapien
142 16 53.3 15 2 Q798W3 9ENTR Q798w3 salmonella
143 16 53.3 16 2 Q6DTV5 HUMAN Q6dtv5 homo sapien
144 16 53.3 16 2 Q9NY32 HUMAN Q9ny32 homo sapien
145 16 53.3 16 2 Q7LZ79 MELGA Q7l279 meleagris g
146 16 53.3 17 2 Q5K151 9DIPT Q5k151 drosophila
147 16 53.3 17 2 Q5K161 9DIPT Q5k161 drosophila
148 16 53.3 17 2 Q4XHA3 PLACH Q4xha3 plasmodium
149 16 53.3 17 2 Q5MBK4 TYMBA Q5mbk4 tympanoctom
150 16 53.3 18 2 Q4Xmw4 PLACH Q4xmw4 plasmodium

RESULT 1
Q6LD79 9MURI PRELIMINARY; PRT; 21 AA.
AC Q6LD79;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Arylhydrocarbon receptor.
GN Name=Ahr;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95218835; PubMed=7704041;
RA Mimura J., Ena M., Sogawa K., Ikawa S., Fujii-Kuriyama Y.;
RT "A complete structure of the mouse Ah receptor gene.";
RL Pharmacogenetics 4:349-354(1994).
DR EMBL; S76844; AAB33978.1; -; Genomic_DNA.
DR MGI; MGI:105043; Ahr.

RESULT 2
Q6LEC9 MOUSE PRELIMINARY; PRT; 21 AA.
AC Q6LEC9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE DNA sequence, exon 1 and 5' end of cds. (Fragment).
GN Name=Ahr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94012821; PubMed=8408082;
RA Schmidt J.V., Carver L.A., Bradfield C.A.;
RT "Molecular characterization of the murine Ahr gene. Organization,
promoter analysis, and chromosomal assignment.";
RL J. Biol. Chem. 268:22203-22209(1993).
DR EMBL; L19757; AAA72026.1; -; Unassigned_DNA.
DR MGI; MGI:105043; Ahr.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005667; C:transcription factor complex; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0003700; P:transcription factor activity; TAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
DR GO; GO:0006805; P:xenobiotic metabolism; TAS.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2380 MW; 98973F72747F4A65 CRC64;

Query Match 83.3%; Score 25; DB 2; Length 21;
Best Local Similarity 100.0%; Pred.No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 5
DB 12 RRRR 16

RESULT 3
Q9UD21 HUMAN PRELIMINARY; PRT; 16 AA.
AC Q9UD21;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Cyclin E-L (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95257942; PubMed=7739542;
RA Ohtsubo M., Theodoras A.M., Schumacher J., Roberts J.M., Pagano M.;
RT "Human cyclin E, a nuclear protein essential for the G1-to-S phase

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RT transition.";
RL Mol. Cell. Biol. 15:2612-2624 (1995).
SQ SEQUENCE 16 AA; 2089 MW; 777EFC69C445E29C CRC64;

Query Match 73.3%; Score 22; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRKR 6
DB 3 KRRER 8

RESULT 4
Q9DEH9_XENLA
ID Q9DEH9_XENLA PRELIMINARY; PRT; 20 AA.
AC Q9DEH9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MCM4 (Fragment).
GN Name=Mcm4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J; TISSUE=Spleen;
RA MEDLINE=20456723; PubMed=11003390; DOI=10.1007/s002510000227;
RX Fujimori A., Araki R., Fukumura R., Ohhata T., Takahashi H.,
RA Kawahara A., Tatsumi K., Abe M.;
RT "Identification of four highly conserved regions in DNA-PKcs.";
RL Immunogenetics 51:965-973 (2000).
DR EMBL; AB016729; BAB19264.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2247 MW; 7F3A0A50B30441AB CRC64;

Query Match 73.3%; Score 22; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KRRKR 6
DB 10 KRRKR 15

RESULT 5
Q7M3Z3_ILLAR
ID Q7M3Z3_ILLAR PRELIMINARY; PRT; 21 AA.
AC Q7M3Z3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sperm chromatin protein 12-2 (Fragment).
OS Illex argentinus (Argentinian squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Oegopsida; Ommastrephidae; Illex.
OX NCBI_TaxID=6628;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90329035; PubMed=2375775;
RA Osadchuk L.A., Levina N.B., Telezhinskaya I.N., Khrapunov S.N.,
RA Berdyshev G.D., Aldanova N.A.;
RT "Primary structure of main nuclear protein from headleg mollusk Illex
RT argentinus and comparison with sperm protein of other animals.";
RL Bioorg. Khim. 16:448-455 (1990).
DR PIR; P00082; P00082.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2931 MW; A9F8D98969174878 CRC64;

Query Match 73.3%; Score 22; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KRRKR 6
DB 2 RRRSR 7

RESULT 6
Q9RF91_PONPY
ID Q9RF91_PONPY PRELIMINARY; PRT; 15 AA.
AC Q9RF91;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469P2021.
GN Name=DKFZp469P2021;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR857270; CAH89566.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 15 AA; 1788 MW; 530A15F11C204E3A CRC64;

Query Match 70.0%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 8 KRRKQ 12

RESULT 7
O35411_MOUSE
ID O35411_MOUSE PRELIMINARY; PRT; 15 AA.
AC O35411;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta III spectrin (Fragment).
GN Name=Spnb3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole embryo;
RX MEDLINE=99045654; PubMed=9826670; DOI=10.1073/pnas.95.24.14158;
RA Starkewich M.C., Tee W.T., Peters L.L., Ch'ng Y., John K.M.,
RA Stabach P.R., Devorajan P., Morrow J.S., Lux S.E.;
RT "A widely expressed betaIII spectrin associated with Golgi and
RT cytoplasmic vesicles.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14158-14163 (1998).
DR EMBL; AF026489; AAC79505.1; -; mRNA.
DR MGI; MGI:1313261; Spnb3.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 2029 MW; CAF6B165F69F1AA8 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;

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Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 2 REREKR 7

RESULT 8
Q76N52 HUMAN
ID Q76N52 HUMAN PRELIMINARY; PRT; 17 AA.
AC Q76N52;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Ribosomal protein L41 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98248690; PubMed=9582194;
RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes.";
RL Genome Res. 8:509-523(1998).
DR EMBL; AB007186; BAA28285.1; -; Genomic_DNA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2385 MW; 1990BBE3EEA7E344 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 6 RKRRMR 11

RESULT 9
Q9UDB7 HUMAN
ID Q9UDB7 HUMAN PRELIMINARY; PRT; 19 AA.
AC Q9UDB7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE CD8 BETA chain isoform S BETA1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170376; PubMed=8436166;
RA DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
RT "Transcriptional diversity at the duplicated human CD8 beta loci.";
RL Eur. J. Immunol. 23:320-326(1993).
SQ SEQUENCE 19 AA; 2527 MW; D1405FE2CEEB4419 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 5 RRRRAR 10

RESULT 10
Q8TOY5 APIME
ID Q8TOY5 APIME PRELIMINARY; PRT; 19 AA.
AC Q8TOY5;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE UORP.
GN Name=Dop2;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98194783; PubMed=9535160;
RA Ebert P.R., Rowland J.E., Toma D.P.;
RT "Isolation of seven unique biogenic amine receptor clones from the
RT honey bee by library scanning.";
RL Insect Mol. Biol. 7:151-162(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Brain mushroom bodies;
RX MEDLINE=22602973; PubMed=12717701; DOI=10.1002/neu.10209;
RA Humphries M.A., Mustard J.A., Hunter S.J., Mercer A., Ward V.,
RA Ebert P.R.;
RT "Invertebrate D2 type dopamine receptor exhibits age-based plasticity
RT of expression in the mushroom bodies of the honeybee brain.";
RL J. Neurobiol. 55:315-330(2003).
DR EMBL; AF498306; AAM19333.1; -; mRNA.
SQ SEQUENCE 19 AA; 2150 MW; 3EB6B9996DFCC16 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 5 RMRKKK 10

RESULT 11
Q4ZG97_9DELA
ID Q4ZG97_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZG97;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C4 HC;
RA Sabouri A.H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus Type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211219; BAD95666.1; -; Genomic_DNA.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 1 RKRRKR 6
```

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Db 10 RSQRKR 15

RESULT 12
Q4ZGB1_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZGB1;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C7 HC;
RA Sabouri A.H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211200; BAD95652.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 10 RSQRKR 15

RESULT 13
Q4ZGB2_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZGB2;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2 HAM;
RA Sabouri A.H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211199; BAD95651.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 10 RSQRKR 15

RESULT 14
Q9UC26_HUMAN PRELIMINARY; PRT; 21 AA.
AC Q9UC26;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Stromelysin-3 zymogen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95265105; PubMed=7746327; DOI=10.1038/375244a0;
RA Pei D., Weiss S.J.;
RT "Furin-dependent intracellular activation of the human Stromelysin-3
RT zymogen.";
RL Nature 375:244-247(1995).
SQ SEQUENCE 21 AA; 2300 MW; BE8C224E96D4B9D6 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 12 RNRQKR 17

RESULT 15
Q9JG23_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9JG23;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RX DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Tanaka T., Miyakawa Y., Mayumi M.;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RT "Circular double-stranded forms of TT virus DNA in the liver.";
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040786; BAA94205.1; -; Genomic_DNA.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 3001 MW; 969C86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 8 RTRRRR 13

RESULT 16
Q9JG26_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9JG26;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
```

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OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RX DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RA Tanaka T., Miyakawa Y., Mayumi M.;
RT "Helicobacter pylori: estimates of clock rates, recombination size and
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040782; BAA94202.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 2922 MW; 953F86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 8 RTRRR 13

RESULT 17
Q9UG30_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9UG30;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RX DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RA Tanaka T., Miyakawa Y., Mayumi M.;
RT "Circular double-stranded forms of TT virus DNA in the liver.";
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040778; BAA94198.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 3001 MW; 969C86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 8 RTRRR 13

RESULT 18
Q8VN85_HELPY PRELIMINARY; PRT; 10 AA.
AC Q8VN85;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Urease accessory protein.
GN Name=uref;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NQ267;
RX MEDLINE=21625040; PubMed=11742075; DOI=10.1073/pnas.251396098;
RA Falush D., Kraft C., Taylor N.S., Correa P., Fox J.G., Achtman M.,
RA Suerbaum S.;
RT "Recombination and mutation during long-term gastric colonization by
RT Helicobacter pylori: estimates of clock rates, recombination size and
RT minimal age.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061(2001).
DR EMBL; AJ418329; CAD11229.1; -; Genomic_DNA.
SQ SEQUENCE 10 AA; 1329 MW; 81E8020403332411 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 4 RKRRKR 9

RESULT 19
Q4GX76_9CUCU PRELIMINARY; PRT; 14 AA.
AC Q4GX76;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Ribosomal protein L4le (Fragment).
GN Name=rpl4le;
OS Curculio glandium.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Curculionidae; Curculioninae; Curculionini; Curculio.
OX NCBI_TaxID=197013;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Longhorn S.J., Vogler A.P.;
RT "Ribosomal proteins of Coleoptera.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AM049147; CAJ17447.1; -; mRNA.
KW Ribosomal protein.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1912 MW; 53EBA7E350113A33 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 6 RKRRKR 11

RESULT 20
Q8HYW9_BOVIN PRELIMINARY; PRT; 19 AA.
AC Q8HYW9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Calcium channel alpha-2/delta subunit 1 (Fragment).
GN Name=cacna2d1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hostein-Friesian; TISSUE=Leukocyte;
RA Buittkamp J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439531; CAD28621.1; -; Genomic_DNA.
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FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2143 MW; 4B078FAL355E79E1 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRR 4
DB 12 RKRR 15

RESULT 21
QSPU92_BRARE PRELIMINARY; PRT; 19 AA.
AC QSPU92;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE T-cell factor 7 isoform D (Fragment).
GN Name=tcf7;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RX PubMed=15765502; DOI=10.1002/dvdy.20330;
RA Veien E.S., Grierson M.J., Saund R.S., Dorsky R.I.;
RT "Expression pattern of zebrafish tcf7 suggests unexplored domains of
RT Wnt/beta-catenin activity.";
RL Dev. Dyn. 233:233-239(2005).
DR EMBL; AY825027; AAV84017.1; -; mRNA.
DR ZFIN; ZDB-GENE-050222-4; tcf7.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2239 MW; 30C5948AC4B9B9A2 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RKRR 6
DB 1 RKRR 4

RESULT 22
Q66MT0_9HIV1 PRELIMINARY; PRT; 19 AA.
AC Q66MT0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Herring B.L., Grant R.M., Delwart E.L.;
RT "No superinfection among seroconcordant couples after well-defined
RT exposure.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF686105; AAU05411.1; -; Genomic_RNA.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2209 MW; D23D5538822A2ED0 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;

Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRR 6
DB 8 RQRRT 13

RESULT 23
Q4YAE2_PLABE PRELIMINARY; PRT; 20 AA.
AC Q4YAE2;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401699.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos P.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01007113; CAI05279.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2358 MW; 75EAD8B63E5C6C5A CRC64;

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKRR 5
DB 6 RKRR 9

RESULT 24
TKNC_CARAU STANDARD; PRT; 21 AA.
AC P25421;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carassin.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91162221; PubMed=2002352;
RA Conlon J.M., O'Harte F., Peter R.E., Kah O.;
RT "Carassin: a tachykinin that is structurally related to neuropeptide-
RT gamma from the brain of the goldfish.";
RL J. Neurochem. 56:1432-1436(1991).
CC -! FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; JH0361; JH0361.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD_RES 21 21 Methionine amide.
SQ SEQUENCE 21 AA; 2369 MW; 1460DC6C5B097A29 CRC64;

Query Match 66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
Db 9 RKRRK 13

RESULT 25
Q7M3M1 HEMPU
ID Q7M3M1 HEMPU PRELIMINARY; PRT; 21 AA.
AC Q7M3M1
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Non-W chromodomain helicase DNA binding protein (W-linked chromodomain
DE helicase DNA binding protein) (Fragment).
OS Histone H1 (Fragment).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemichentrotus.
ON NCBI_TaxID=7650;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91115778; PubMed=2126010;
RA Suzuki M., Sugiura M., Ebashi S.;
RT "Sea urchin protease specific to the SPKK motif in histone.";
RL J. Biochem. 108:347-355(1990).
DR PIR; PS0146; PS0146.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2378 MW; 0B32BA52D8DD06D7 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
Db 13 RSRRK 17

RESULT 26
Q662J7 BORG
ID Q662J7 BORG PRELIMINARY; PRT; 21 AA.
AC Q662J7
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BG0166;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
ON NCBI_TaxID=29519;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PBI;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suehnel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07024.1; -; Genomic DNA.
SQ SEQUENCE 21 AA; 2526 MW; 7FCA6CC18506B3D3 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 6
Db 10 QKKKKR 15

RESULT 27
Q9DD39 NIPNI
ID Q9DD39 NIPNI PRELIMINARY; PRT; 21 AA.
AC Q9DD39
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Non-W chromodomain helicase DNA binding protein (W-linked chromodomain
DE helicase DNA binding protein) (Fragment).
OS Name=non-W CHD; Synonyms=W-linked CHD;
OS Nipponia nippon (Crested ibis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;
OC Nipponia.
ON NCBI_TaxID=128390;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Arai Y., Ishii S., Kikuchi M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049444; BAB15805.1; -; Genomic DNA.
DR EMBL; AB049443; BAB15804.1; -; Genomic DNA.
DR GO; GO:0004386; F:helicase activity; IEA.
KW Helicase.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2588 MW; C8E13B3B1AD353E3 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 6
Db 4 RKRRK 9

RESULT 28
Q9PRZ3 ONCMY
ID Q9PRZ3 ONCMY PRELIMINARY; PRT; 21 AA.
AC Q9PRZ3
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Neuropeptide-gamma (NP-gamma) (Tachykinin homolog).
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ON NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94056890; PubMed=7694488;
RA Jensen J., Olson K.R., Conlon J.M.;
RT "Primary structures and effects on gastrointestinal motility of

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RT tachykinins from the rainbow trout.";
RL Am. J. Physiol. 265:R804-R810(1993).
DR GO: GO:0005102; P:receptor binding; IEA.
DR GO: GO:0007218; P:neuropeptide signaling pathway; IEA.
DR GO: GO:0007268; P:synaptic transmission; IEA.
DR GO: GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro: IPR002040; TachyNeurokinin.
DR Pfam: PF02202; Tachykinin_1.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
KW Neuropeptide; Tachykinin.
SQ SEQUENCE 21 AA; 2385 MW; 080CAC6E36997A29 CRC64;

Query Match          66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 9 RKRRK 13

RESULT 29
Q70Y78 9LAMI
ID Q70Y78 9LAMI PRELIMINARY; PRT; 10 AA.
AC Q70Y78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Ribosomal protein (Fragment).
GN Name=rpal6;
OS Plectranthus parishii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
OX NCBI_TaxID=204190;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505390; CAD45510.1; -; Genomic DNA.
DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 10 10
FT NON_TER 1
SQ SEQUENCE 10 AA; 1299 MW; 87C8C86723241411 CRC64;

Query Match          63.3%; Score 19; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 2 RTRRK 6

RESULT 30
Q70Y85 9LAMI
ID Q70Y85 9LAMI PRELIMINARY; PRT; 11 AA.
AC Q70Y85;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Ribosomal protein (Fragment).
GN Name=rpal6;
OS Platosoma rubrum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

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OC lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platosoma.
OX NCBI_TaxID=204176;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505373; CAD45494.1; -; Genomic DNA.
DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 11 11
FT NON_TER 1
SQ SEQUENCE 11 AA; 1430 MW; 7397DC9867232414 CRC64;

Query Match          63.3%; Score 19; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 2 RTRRK 6

Search completed: April 13, 2006, 08:49:02
Job time : 232 secs

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